



83	7	2.6	282	20	RAY08328	M. grisea THNR pro	156	34	22	ABB27825	Human peptide #476
84	7	2.6	283	20	ABP0501	Staphylococcus epi	157	34	22	ABB32996	Peptide #502 enco
85	7	2.6	286	22	AAU36267	Pseudomonas aerugi	158	34	22	ABB42614	Peptide #10120 enc
86	7	2.6	298	21	AGB4787	Arabidopsis thalia	159	34	22	ABB18469	Protein #468 enco
87	7	2.6	298	21	AGB50312	Arabidopsis thalia	160	34	22	ABB37794	Human brain expres
88	7	2.6	308	22	AGB1589	S. epidermidis ope	161	34	22	AAAG53794	Human brain expres
89	7	2.6	311	23	ABP40326	Staphylococcus epi	162	34	22	AAAG66180	Human bone marrow
90	7	2.6	315	21	AGB50311	Arabidopsis thalia	163	34	22	AAAM76319	Human bone marrow
91	7	2.6	316	21	AGB16294	Eucalyptus grandis	164	34	22	AAAM14051	Peptide #485 enco
92	7	2.6	316	21	AGB16321	Pinus radiata anne	165	34	22	AAAM26457	Peptide #473 enco
93	7	2.6	316	21	AGB24786	Arabidopsis thalia	166	34	22	AAAM01791	Human peptide enco
94	7	2.6	316	22	ABG65730	Annexin-like prote	167	34	22	ABG35830	H. pylori cytoplas
95	7	2.6	317	22	ABG65195	Drosophila melanog	168	37	18	AAW20245	Human prostate can
96	7	2.6	346	22	ABG71575	Drosophila melanog	169	37	22	AAU22783	Human reproductive
97	7	2.6	363	21	AGB08399	Arabidopsis thalia	170	37	22	AAAG4766	Human liver peptid
98	7	2.6	372	20	AAW8301	E. coli O157 anti	171	38	22	ABG57627	Human secreted pro
99	7	2.6	372	20	AAW8301	E. coli O111 anti	172	39	21	AAAB44596	Human secreted pro
100	7	2.6	372	23	ABG34138	Antibody productio	173	40	21	AAAB28737	Human protective s
101	7	2.6	384	21	AGB08398	Arabidopsis thalia	174	41	23	ABBA4709	Novel human diagno
102	7	2.6	387	22	ABG64058	Drosophila melanog	175	42	22	ABG29936	Novel human diagno
103	7	2.6	407	22	ABG1652	Drosophila melanog	176	44	19	AAW70327	Novel human diagno
104	7	2.6	426	22	ABG15281	Novel human diagno	177	46	22	ABG28111	Novel human diagno
105	7	2.6	429	21	AAI53802	47.7 kDa insectici	178	47	20	AAW73408	Human secreted pro
106	7	2.6	429	21	AAI53804	Insectical protein	179	48	20	AAW30889	Human secreted pro
107	7	2.6	439	21	AAI53808	Insectical protein	180	49	22	ABG57527	Human liver peptid
108	7	2.6	452	22	AGB70913	S cerevisiae apopt	181	49	22	ABG42096	Peptide #3602 enco
109	7	2.6	480	22	ABG60578	Drosophila melanog	182	49	22	AAAG52976	Human brain expres
110	7	2.6	481	21	AAI58020	Aspergillus sojae	183	49	22	AAAG5789	Human bone marrow
111	7	2.6	481	24	ABU52604	Human NOVX protein	184	49	22	AAAG35899	Peptide #9936 enco
112	7	2.6	496	20	AAW85957	Aspergillus oryzae	185	49	23	ABG45259	Human peptide enco
113	7	2.6	496	20	AAW85957	Aspergillus oryzae	186	50	21	AAAG56198	Arabidopsis thalia
114	7	2.6	496	20	AAW85958	Aspergillus oryzae	187	50	21	AAAG33320	SIPI minimal Smad
115	7	2.6	550	22	ABG60941	Drosophila melanog	188	52	22	AAAG5784	Propionibacterium
116	7	2.6	569	22	AAU38295	Salmonella typhi c	189	53	19	AAU21383	Human HUPF-1 mutan
117	7	2.6	573	21	AAI74962	Neisseria meningit	190	53	23	ABP35441	Human isomerase-li
118	7	2.6	575	21	AAI74961	Neisseria meningit	191	54	22	AAW70324	Human bone marrow
119	7	2.6	592	24	ABG30418	Human testis speci	192	54	22	AAAG18163	Peptide #4597 enco
120	7	2.6	592	23	ABU00143	Human novel polype	193	54	22	AAAG5785	Peptide #4467 enco
121	7	2.6	614	20	AAW98112	T-cell membrane pr	194	55	23	ABG39970	Human peptide enco
122	7	2.6	614	20	AAW98113	T-cell membrane pr	195	55	23	ABG39970	Human musculoskele
123	7	2.6	634	22	ABG60004	Drosophila melanog	196	56	22	ABG03427	Novel human muscu
124	7	2.6	643	23	ABP41524	Human ovarian anti	197	56	22	ABU12721	Human liver peptid
125	7	2.6	822	19	AAW41943	Human OC-116 kDa p	198	56	22	AAU57140	Propionibacterium
126	7	2.6	822	23	ABG81811	Human OC-116 kDa p	199	56	22	AAU57140	Propionibacterium
127	7	2.6	824	23	AAU81516	Herbicidally activ	200	56	22	ABG38700	Peptide #1351 enco
128	7	2.6	858	23	ABG92904	Pseudomonas aerugi	201	56	22	ABG38700	Peptide #1388 enco
129	7	2.6	908	22	AAU36254	Bifidobacterium lo	202	56	22	ABG33882	Protein #1322 enco
130	7	2.6	1039	23	ABP66060	Drosophila melanog	203	56	22	AAAG4648	Human brain expres
131	7	2.6	1469	22	ABG68168	Drosophila melanog	204	56	22	AAAG4648	Human bone marrow
132	7	2.6	1778	23	ABG47314	Listeria monocytog	205	56	22	AAAG4914	Peptide #1348 enco
133	7	2.6	2705	22	AAW90772	Human shear stress	206	56	22	AAAG27343	Peptide #1322 enco
134	6	2.2	9	20	AAW81038	Melanoma associate	207	56	22	AAAG2640	Human prostate tum
135	6	2.2	9	22	AAW81038	Melanoma associate	208	56	22	ABG36709	Human prostate tum
136	6	2.2	11	22	AAW47531	OspA TC epitope ho	209	57	20	AAI74221	Propionibacterium
137	6	2.2	14	21	AAW99412	Staphylokinase T-C	210	58	22	AAU59787	Propionibacterium
138	6	2.2	17	22	AAW99401	Escherichia coli C	211	58	22	AAU67783	Human EST encoded
139	6	2.2	20	15	AAW45544	Staphylokinase var	212	58	22	AAAG4155	Human ORFX protein
140	6	2.2	20	16	AAW82493	Cry j I pollen all	213	59	23	ABP11103	Arabidopsis thalia
141	6	2.2	20	20	AAW82493	Cry j I Japanese CJ	214	61	21	AAAG56893	Human liver peptid
142	6	2.2	20	22	AAW29017	CJ linker library	215	62	22	ABG30025	Human liver peptid
143	6	2.2	21	22	ABG94204	Novel human diagno	216	62	22	ABG33255	Peptide #2634 enco
144	6	2.2	30	21	AAW97234	FIV gp36 envelope	217	62	22	ABG33255	Peptide #2634 enco
145	6	2.2	31	19	AAW69836	Human neurofilamen	218	62	22	ABG33255	Peptide #2634 enco
146	6	2.2	31	22	AAW31486	Novel human secret	219	62	22	ABG33255	Peptide #2634 enco
147	6	2.2	32	22	ABG56572	Human liver peptid	220	62	22	ABG33255	Peptide #2634 enco
148	6	2.2	32	22	ABG41303	Peptide #11809 enc	221	62	22	ABG33255	Peptide #2634 enco
149	6	2.2	32	22	ABG21165	Protein #5164 enco	222	62	22	ABG33255	Peptide #2634 enco
150	6	2.2	32	22	AAW65340	Human brain expres	223	62	22	AAAG5987	Protein #2581 enco
151	6	2.2	32	22	AAW78035	Human bone marrow	224	62	22	AAAG5987	Human brain expres
152	6	2.2	32	22	AAW21926	Peptide #8360 enco	225	62	22	AAAG5987	Human bone marrow
153	6	2.2	32	22	AAW38256	Peptide #12293 enc	226	62	22	AAAG5987	Peptide #2808 enco
154	6	2.2	34	22	ABG47848	Human liver peptid	227	62	22	AAAG5987	Peptide #2808 enco
155	6	2.2	34	22	ABG58029	Human liver peptid	228	62	22	AAAG5987	Peptide #2808 enco

229	6	2.2	62	22	AA03901	Peptide #2583 enco	302	111	19	AAW61227	Streptococcus pneu
230	6	2.2	62	23	ABG37912	Human peptide enco	303	111	23	ABP54646	S. pneumoniae SP10
231	6	2.2	62	23	ABG41385	Human peptide enco	304	112	23	ABY36822	Amino acid sequenc
232	6	2.2	63	22	AAU63622	Propionibacterium	305	113	21	AGI15003	Arabidopsis thalia
233	6	2.2	63	22	ABP04955	Human ORFX protein	306	113	21	ABG11726	Novel human diagno
234	6	2.2	65	22	AGG9566	ERA binding domain	307	114	21	AGG44971	Zea mays protein f
235	6	2.2	66	21	AGS6892	Arabidopsis thalia	308	117	21	AGI2552	Zea mays protein f
236	6	2.2	66	23	ABP31177	Human histone-like	309	117	22	AAI2552	Macaque EST encode
237	6	2.2	67	22	AGS9870	Human liver peptid	310	117	22	AAI2554	Human RNA polymera
238	6	2.2	67	22	AAU42309	Propionibacterium	311	117	22	AAI49273	C glutamic prote
239	6	2.2	67	22	ABBA4475	Peptide #11981 enc	312	118	22	AAI92489	Humanised MAB heav
240	6	2.2	68	22	AAH05991	Human haematologic	313	119	14	AAI22240	Humanised MAB heav
241	6	2.2	68	22	AAH18197	Human haematologic	314	119	14	AAI22243	Humanised MAB heav
242	6	2.2	69	21	AGI17274	Arabidopsis thalia	315	119	14	AAI22244	Mature heavy chain
243	6	2.2	70	22	AAU57758	Propionibacterium	316	119	18	AAI27144	Humanised ABL 364
244	6	2.2	71	21	ABP64804	Human protein SEQ	317	119	22	AAI87570	Human AFP protein
245	6	2.2	72	21	AGI10911	Arabidopsis thalia	318	121	21	AGI1441	Zea mays protein f
246	6	2.2	72	23	ABU05844	M. tuberculosis an	319	121	21	AGI4980	Corynebacterium g1
247	6	2.2	73	22	AAU57812	Propionibacterium	320	121	21	ABY79281	Human glycoprotein
248	6	2.2	75	21	AGI32969	Arabidopsis thalia	321	121	23	ABP13114	Human ORFX ORF938
249	6	2.2	75	22	AAU39235	Propionibacterium	322	122	21	AAI41174	Arabidopsis thalia
250	6	2.2	75	22	AAU46232	Propionibacterium	323	122	21	AGI60092	Human ORFX protein
251	6	2.2	75	22	ABY5913	Human nervous syst	324	122	21	ABP04840	Staphylokinase SAK
252	6	2.2	75	23	ABP03061	Human ORFX protein	325	123	21	AAI75507	Neisseria gonorrhoe
253	6	2.2	76	21	ABY59063	Breast and ovarian	326	123	21	AAI75508	Neisseria meningit
254	6	2.2	76	22	ABP04887	Human ORFX protein	327	123	21	AAI75509	Neisseria meningit
255	6	2.2	78	22	AAU54776	Propionibacterium	328	123	21	ABP26118	Streptococcus poly
256	6	2.2	78	22	AAU56637	Propionibacterium	329	126	13	AAI25458	Thrombolytic pepti
257	6	2.2	78	22	AGI74430	Human colon cancer	330	126	18	AAI20377	H. pylori surface
258	6	2.2	79	22	AAU39106	Propionibacterium	331	126	18	AGI23354	Zea mays protein f
259	6	2.2	80	21	AGI17273	Arabidopsis thalia	332	126	21	AAI12354	S. pneumoniae type
260	6	2.2	81	23	ABP09889	Human ORFX protein	333	126	24	ABU1062	Staphylokinase SAK
261	6	2.2	82	22	AGI75788	Human colon cancer	334	127	14	AAI39151	Human liver peptid
262	6	2.2	84	22	AGI64880	Murine protein SEQ	335	127	22	ABG52883	Human ORFX protein
263	6	2.2	84	22	AGI64883	Murine protein SEQ	336	127	22	ABY38035	Staphylokinase SAK
264	6	2.2	84	23	ABP34514	Human ORFX protein	337	127	22	ABY23287	Human bone marrow
265	6	2.2	88	22	AGI75162	Human colon cancer	338	127	22	AAI58665	Human brain expres
266	6	2.2	89	22	AAO02868	Human polypeptide	339	127	22	AAI17171	Peptide #5343 enco
267	6	2.2	89	23	ABP01213	Human ORFX protein	340	127	22	AAI18909	Peptide #5489 enco
268	6	2.2	90	18	AAI33889	Flea saliva protei	341	127	22	AAI31452	Human peptide enco
269	6	2.2	90	19	AAI22363	Flea saliva protei	342	127	23	ABG40968	Human polypeptide
270	6	2.2	90	22	AAU61776	Propionibacterium	343	127	23	ABY89076	Deduced from Lelys
271	6	2.2	91	21	ABY14137	Bordetella pertuss	344	128	13	AAI29946	PRRS virus (Spain)
272	6	2.2	91	21	AGI10910	Arabidopsis thalia	345	128	16	AAI74643	PRRS virus (Spain)
273	6	2.2	91	21	AGI56246	Arabidopsis thalia	346	128	17	AAI94706	PRRS virus (Spain)
274	6	2.2	91	23	ABP07609	Human ORFX protein	347	128	17	AAI88707	Porcine reproducti
275	6	2.2	92	22	ABG18734	Novel human diagno	348	128	17	AAI68456	PRRS isolate Tole
276	6	2.2	92	23	ABP06385	Human ORFX protein	349	128	20	AAI84335	Protein N of PRRSV
277	6	2.2	93	21	ABY40664	Human ORFX protein	350	128	22	ABY59767	Human liver peptid
278	6	2.2	94	22	AAU56996	Propionibacterium	351	128	22	AAI48122	Propionibacterium
279	6	2.2	95	23	ABY5791	Lactococcus lactis	352	128	22	AAI65460	Human brain expres
280	6	2.2	96	22	ABG14837	Novel human diagno	353	128	22	AAI38366	Peptide #12403 enc
281	6	2.2	96	22	AAO09550	Human polypeptide	354	128	22	AAU07139	Porcine reproducti
282	6	2.2	96	23	ABY10043	Human glucose tran	355	128	23	ABG96503	PRRS virus ORF7 pr
283	6	2.2	97	23	ABY97493	Novel human protei	356	128	23	ABG47145	Human peptide enco
284	6	2.2	99	23	ABP04383	Human ORFX protein	357	128	24	AAU76142	Porcine reproducti
285	6	2.2	101	23	ABP34284	Human kinase-like	358	128	24	ABY70395	Amino acid sequenc
286	6	2.2	101	23	ABP06196	Human ORFX protein	359	129	22	AAU59978	Propionibacterium
287	6	2.2	102	22	AAU07435	Flock house virus	360	129	22	ABY15536	Human nervous syst
288	6	2.2	102	23	AAU79657	Parietaria judaica	361	129	22	AAU18302	Human endocrine po
289	6	2.2	102	23	AAU79658	Parietaria judaica	362	130	21	AAI26892	Zea mays protein f
290	6	2.2	103	23	ABP39049	Staphylococcus epi	363	130	22	ABY1855	Drosophila melanog
291	6	2.2	104	22	AAU48120	Propionibacterium	364	131	17	AAI06934	CagI locus product
292	6	2.2	104	22	AAU60036	Propionibacterium	365	131	18	AAI20697	H. pylori putative
293	6	2.2	104	22	AAH08099	Human haematologic	366	131	20	AAI25608	Parietaria sp. all
294	6	2.2	104	22	AAH1968	Human haematologic	367	131	20	AAI25606	Parietaria sp. all
295	6	2.2	106	21	AGI58834	Arabidopsis thalia	368	133	23	ABP12750	Human RNA polymera
296	6	2.2	108	21	AGI54610	Zea mays protein f	369	135	21	AAI01298	Altered staphyloki
297	6	2.2	109	7	AAI60796	Fragment of sak ge	370	136	17	AAI03079	Staphylokinase der
298	6	2.2	109	21	AAI27841	Sequence homology	371	136	17	AAI03077	Staphylokinase der
299	6	2.2	109	21	AAI27842	Protein fragment e	372	136	17	AAI03082	Staphylokinase der
300	6	2.2	110	19	AAI98574	H. pylori GHPO 27	373	136	17	AAI03083	Staphylokinase der
301	6	2.2	110	23	ABP00777	Human ORFX protein	374	136	17	AAI03080	Staphylokinase der

375	6	2.2	136	17	AAW03097	Staphylokinase der	448	6	2.2	136	20	AAV15049	Staphylokinase var
376	6	2.2	136	17	AAW03081	Staphylokinase der	449	6	2.2	136	20	AAV15050	Staphylokinase var
377	6	2.2	136	17	AAW03074	Staphylokinase der	450	6	2.2	136	20	AAV15060	Staphylokinase var
378	6	2.2	136	17	AAW03075	Staphylokinase der	451	6	2.2	136	20	AAV15061	Staphylokinase var
379	6	2.2	136	17	AAW03076	Staphylokinase der	452	6	2.2	136	20	AAV15027	Staphylokinase var
380	6	2.2	136	17	AAW03095	Staphylokinase der	453	6	2.2	136	20	AAV15032	Staphylokinase var
381	6	2.2	136	17	AAW03096	Staphylokinase der	454	6	2.2	136	20	AAV15023	Staphylokinase var
382	6	2.2	136	17	AAW03098	Staphylokinase der	455	6	2.2	136	20	AAV15038	Staphylokinase var
383	6	2.2	136	17	AAW03099	Staphylokinase der	456	6	2.2	136	20	AAV15024	Staphylokinase var
384	6	2.2	136	17	AAW03100	Staphylokinase der	457	6	2.2	136	20	AAV15054	Staphylokinase var
385	6	2.2	136	17	AAW03101	Staphylokinase der	458	6	2.2	136	20	AAV15025	Staphylokinase var
386	6	2.2	136	17	AAW03102	Staphylokinase der	459	6	2.2	136	20	AAV15039	Staphylokinase var
387	6	2.2	136	17	AAW03071	Wild-type staphylo	460	6	2.2	136	20	AAV15026	Staphylokinase var
388	6	2.2	136	17	AAW03072	Staphylokinase der	461	6	2.2	136	20	AAV15027	Staphylokinase var
389	6	2.2	136	17	AAW03073	Staphylokinase der	462	6	2.2	136	20	AAV15040	Staphylokinase var
390	6	2.2	136	17	AAW03093	Staphylokinase der	463	6	2.2	136	20	AAV15028	Staphylokinase var
391	6	2.2	136	17	AAW03090	Staphylokinase der	464	6	2.2	136	20	AAV15055	Staphylokinase var
392	6	2.2	136	17	AAW03094	Staphylokinase der	465	6	2.2	136	20	AAV15029	Staphylokinase var
393	6	2.2	136	17	AAW03103	Staphylokinase der	466	6	2.2	136	20	AAV15041	Staphylokinase var
394	6	2.2	136	17	AAW03104	Staphylokinase der	467	6	2.2	136	20	AAV15030	Staphylokinase var
395	6	2.2	136	17	AAW03087	Staphylokinase der	468	6	2.2	136	20	AAV15007	Staphylokinase var
396	6	2.2	136	17	AAW03088	Staphylokinase der	469	6	2.2	136	20	AAV15013	Staphylokinase var
397	6	2.2	136	17	AAW03089	Staphylokinase der	470	6	2.2	136	20	AAV15008	Staphylokinase var
398	6	2.2	136	17	AAW03091	Staphylokinase der	471	6	2.2	136	20	AAV15009	Staphylokinase var
399	6	2.2	136	17	AAW03092	Staphylokinase der	472	6	2.2	136	20	AAV15014	Staphylokinase var
400	6	2.2	136	17	AAW03084	Staphylokinase der	473	6	2.2	136	20	AAV15034	Staphylokinase var
401	6	2.2	136	17	AAW03085	Staphylokinase der	474	6	2.2	136	20	AAV15015	Staphylokinase var
402	6	2.2	136	17	AAW03086	Wild-type staphylo	475	6	2.2	136	20	AAV15016	Staphylokinase var
403	6	2.2	136	17	AAW03027	Staphylokinase der	476	6	2.2	136	20	AAV15035	Staphylokinase var
404	6	2.2	136	17	AAW03028	Staphylokinase der	477	6	2.2	136	20	AAV15018	Staphylokinase var
405	6	2.2	136	17	AAW03029	Staphylokinase der	478	6	2.2	136	20	AAV15019	Staphylokinase var
406	6	2.2	136	17	AAW03030	Staphylokinase der	479	6	2.2	136	20	AAV15036	Staphylokinase var
407	6	2.2	136	17	AAW03031	Staphylokinase der	480	6	2.2	136	20	AAV15020	Staphylokinase var
408	6	2.2	136	17	AAW44689	Staphylokinase mut	481	6	2.2	136	20	AAV15053	Staphylokinase var
409	6	2.2	136	19	AAW44696	Staphylokinase fro	482	6	2.2	136	20	AAV15021	Staphylokinase var
410	6	2.2	136	19	AAW44690	Staphylokinase mut	483	6	2.2	136	20	AAV15010	Staphylokinase var
411	6	2.2	136	19	AAW44691	Staphylokinase mut	484	6	2.2	136	20	AAV15002	Staphylokinase var
412	6	2.2	136	19	AAW44692	Staphylokinase mut	485	6	2.2	136	20	AAV15003	Staphylokinase var
413	6	2.2	136	19	AAW44693	Staphylokinase mut	486	6	2.2	136	20	AAV15011	Staphylokinase var
414	6	2.2	136	19	AAW44694	Staphylokinase mut	487	6	2.2	136	20	AAV15004	Staphylokinase var
415	6	2.2	136	19	AAW44695	Staphylokinase mut	488	6	2.2	136	20	AAV15032	Staphylokinase var
416	6	2.2	136	20	AAV15078	Staphylokinase var	489	6	2.2	136	20	AAV15005	Staphylokinase var
417	6	2.2	136	20	AAV15079	Staphylokinase var	490	6	2.2	136	20	AAV15012	Staphylokinase var
418	6	2.2	136	20	AAV15080	Staphylokinase var	491	6	2.2	136	20	AAV15006	Staphylokinase var
419	6	2.2	136	20	AAV15082	Staphylokinase var	492	6	2.2	136	20	AAV15033	Staphylokinase var
420	6	2.2	136	20	AAV15062	Staphylokinase var	493	6	2.2	136	20	AAV01232	S. aureus staphylo
421	6	2.2	136	20	AAV15063	SakSTAR (K57A, E58	494	6	2.2	136	21	AAO44284	Staphylococcus aur
422	6	2.2	136	20	AAV15064	Staphylokinase var	495	6	2.2	136	21	AAO04323	Arabidopsis thalia
423	6	2.2	136	20	AAV15065	SakSTAR (K35A, E65	496	6	2.2	136	21	AAO08768	Arabidopsis thalia
424	6	2.2	136	20	AAV15066	Staphylokinase var	497	6	2.2	136	21	AAO22478	Arabidopsis thalia
425	6	2.2	136	20	AAV15067	SakSTAR (B65D, K74	498	6	2.2	136	21	AAO43813	Arabidopsis thalia
426	6	2.2	136	20	AAV15068	SakSTAR (B65D, K74	499	6	2.2	136	21	AAO44415	Arabidopsis thalia
427	6	2.2	136	20	AAV15069	Staphylokinase var	500	6	2.2	136	21	AAO51295	Arabidopsis thalia
428	6	2.2	136	20	AAV15070	Staphylokinase var	501	6	2.2	136	21	AAO53099	Arabidopsis thalia
429	6	2.2	136	20	AAV15071	SakSTAR (K35A, E65	502	6	2.2	136	21	AAO53143	Arabidopsis thalia
430	6	2.2	136	20	AAV15072	Staphylokinase var	503	6	2.2	136	21	AAO53145	Arabidopsis thalia
431	6	2.2	136	20	AAV15073	Staphylokinase var	504	6	2.2	136	21	AAO58019	Arabidopsis thalia
432	6	2.2	136	20	AAV15074	Staphylokinase var	505	6	2.2	136	21	AAO01297	Wild type staphylo
433	6	2.2	136	20	AAV15075	Staphylokinase var	506	6	2.2	136	21	AAO99594	Staphylococcus pia
434	6	2.2	136	20	AAV15076	Staphylokinase var	507	6	2.2	136	21	AAV50871	Staphylococcus aur
435	6	2.2	136	20	AAV15077	Staphylokinase var	508	6	2.2	136	22	AAO99421	Staphylokinase (Sa
436	6	2.2	136	20	AAV15078	Staphylokinase var	509	6	2.2	136	22	AAO61908	S. aureus staphylo
437	6	2.2	136	20	AAV15042	Staphylokinase var	510	6	2.2	136	22	AAO61909	S. aureus staphylo
438	6	2.2	136	20	AAV15056	Staphylokinase var	511	6	2.2	136	23	AAO47321	Human dipeptide am
439	6	2.2	136	20	AAV15043	Staphylokinase var	512	6	2.2	136	23	AAO47321	Sak glucokinase
440	6	2.2	136	20	AAV15044	Staphylokinase var	513	6	2.2	137	14	AAO39154	Staphylokinase Sak
441	6	2.2	136	20	AAV15057	Staphylokinase var	514	6	2.2	137	14	AAO39148	Staphylokinase Sak
442	6	2.2	136	20	AAV15045	Staphylokinase var	515	6	2.2	137	14	AAO39149	Staphylokinase Sak
443	6	2.2	136	20	AAV15046	Staphylokinase var	516	6	2.2	137	14	AAO39150	Staphylokinase Sak
444	6	2.2	136	20	AAV15058	Staphylokinase var	517	6	2.2	137	14	AAO39153	Staphylokinase Sak
445	6	2.2	136	20	AAV15047	Staphylokinase var	518	6	2.2	137	18	AAO33888	Flea saliva proteol
446	6	2.2	136	20	AAV15048	Staphylokinase var	519	6	2.2	137	19	AAO82362	Staphylokinase
447	6	2.2	136	20	AAV15059	Staphylokinase var	520	6	2.2	137	20	AAV15051	SakSTAR (B65Q, K74



521	6	2.2	137	20	AAV15001	Staphylokinase gen	594	6	2.2	156	22	AAO05105	Peptide #3787 enco
522	6	2.2	138	14	AAR32242	Chimeric MAB heavy	595	6	2.2	157	21	AAG08767	Arabidopsis thalia
523	6	2.2	138	14	AAR32246	BR55-2 murine IgG3	596	6	2.2	157	21	AAG51262	Arabidopsis thalia
524	6	2.2	138	22	ABG26002	Novel human diagno	597	6	2.2	157	21	AAG53142	Arabidopsis thalia
525	6	2.2	138	22	ABG26008	Novel human diagno	598	6	2.2	157	22	AAG79850	Corynebacterium gl
526	6	2.2	138	22	AAG90088	C glutamicum prote	599	6	2.2	158	11	AAR08285	Thermally stable c
527	6	2.2	138	22	AAB92884	Human protein sequ	600	6	2.2	158	12	AAR12138	Staphylokinase-som
528	6	2.2	139	14	AAR31588	BR55-2 heavy chain	601	6	2.2	158	16	AAR66507	Yeast cytosine-dea
529	6	2.2	139	19	AAW56427	Amino end of the	602	6	2.2	158	21	AAI75142	Arabidopsis thalia
530	6	2.2	140	21	AAW27795	Human secreted pro	603	6	2.2	158	21	AAI75142	Human secreted pro
531	6	2.2	140	21	AAI91355	Human secreted pro	604	6	2.2	158	21	AAI55101	Chimeric cytosine
532	6	2.2	141	22	AAU39297	Propionibacterium	605	6	2.2	158	21	AAI55102	Chimeric cytosine
533	6	2.2	142	21	AAG338250	Arabidopsis thalia	606	6	2.2	158	21	AAI55103	Chimeric cytosine
534	6	2.2	143	22	AAO11085	Human polypeptide	607	6	2.2	158	21	AAI55104	Chimeric cytosine
535	6	2.2	144	22	AAG55785	Arabidopsis thalia	608	6	2.2	161	23	ABA48163	Listeria monocytog
536	6	2.2	144	22	AAG99298	Human ribosomal ph	609	6	2.2	163	12	AAI21337	S aureus Staphylok
537	6	2.2	145	21	AAG04194	Arabidopsis thalia	610	6	2.2	163	13	AAI28844	Staphylokinase (SAK
538	6	2.2	145	21	AAG12733	Arabidopsis thalia	611	6	2.2	163	14	AAI39155	Staphylokinase SAK
539	6	2.2	145	21	AAG23325	Arabidopsis thalia	612	6	2.2	163	16	AAI75207	Recombinant staphy
540	6	2.2	145	22	AAG70734	S cerevisiae apopt	613	6	2.2	163	21	AAG28324	Arabidopsis thalia
541	6	2.2	145	22	AAG70865	C albicans apoptos	614	6	2.2	163	21	AAG78153	Glucokoniase (RG
542	6	2.2	145	23	ABP02820	Human ORF protein	615	6	2.2	163	21	AAG78160	Glucokoniase SAK
543	6	2.2	146	21	AAG15899	Arabidopsis thalia	616	6	2.2	163	21	AAG78161	Glucokoniase RGD
544	6	2.2	146	21	AAG44970	Zea mays proteoin f	617	6	2.2	163	21	AAG78162	Glucokoniase KGD
545	6	2.2	146	22	ABH11411	Human secreted pro	618	6	2.2	163	22	AAU41126	Propionibacterium
546	6	2.2	146	22	AAH81086	Human haematologic	619	6	2.2	163	23	ABJ10991	Yeast selected int
547	6	2.2	146	22	AAH81536	Human haematologic	620	6	2.2	164	18	AAI5254	Human FC99 phospho
548	6	2.2	146	22	AAH25895	Human protein sequ	621	6	2.2	164	18	AAI5258	Rat FC99 phosphory
549	6	2.2	147	23	AAO16108	Glucokoniase-annexi	622	6	2.2	164	21	AAG04322	Arabidopsis thalia
550	6	2.2	148	21	AAG23419	Arabidopsis thalia	623	6	2.2	164	21	AAG12550	Zea mays protein f
551	6	2.2	148	21	AAI99437	Human PRO1508 (UNQ	624	6	2.2	164	21	AAG53098	Arabidopsis thalia
552	6	2.2	148	21	AAI87323	Human signal pepti	625	6	2.2	165	21	AAG33468	Arabidopsis thalia
553	6	2.2	148	22	AAU27620	Human protein AFP6	626	6	2.2	165	21	AAG35506	Arabidopsis thalia
554	6	2.2	148	22	AAU29203	Human PRO polypept	627	6	2.2	166	21	AAI83339	Arabidopsis thalia
555	6	2.2	148	22	AAH23865	Human EST encoded	628	6	2.2	166	21	AAI53144	Arabidopsis thalia
556	6	2.2	148	22	AAH66186	Human angioogenesis	629	6	2.2	169	22	AAH64184	Streptomyces viola
557	6	2.2	148	23	ABH95543	Human PRO1508 prot	630	6	2.2	170	21	AAG67837	Amino acid sequenc
558	6	2.2	148	23	ABH84937	Human PRO1508 prot	631	6	2.2	170	22	AAH67837	Human gastric canc
559	6	2.2	148	24	ABU71291	Human secreted/tra	632	6	2.2	170	22	AAH63541	Protein encoded by
560	6	2.2	148	24	ABU65748	Novel human secret	633	6	2.2	170	22	AAH29192	Arabidopsis transc
561	6	2.2	148	24	ABU65608	Human secreted/tra	634	6	2.2	170	23	AAI93024	Arabidopsis thalia
562	6	2.2	148	24	ABU67585	Human secreted/tra	635	6	2.2	173	21	AAI5501	Human polypeptide
563	6	2.2	148	24	ABU65443	Human PRO polypept	636	6	2.2	173	22	AAH93867	Human clone vpi5.1
564	6	2.2	148	24	ABU58579	Human PRO polypept	637	6	2.2	175	21	AAI95031	Human secreted pro
565	6	2.2	148	24	ABU56115	Human secreted/tra	638	6	2.2	176	19	AAH74849	Human novel secret
566	6	2.2	148	24	ABU57110	Human PRO polypept	639	6	2.2	176	23	ABG95300	Tumour involved ge
567	6	2.2	148	24	ABU10689	Human secreted/tra	640	6	2.2	178	23	ABG79704	Human colon cancer
568	6	2.2	149	21	AAG24388	Arabidopsis thalia	641	6	2.2	179	22	AAH77782	E. coli Lac-YHI-Sa
569	6	2.2	149	21	AAG51576	Arabidopsis thalia	642	6	2.2	179	22	AAH86832	Arabidopsis thalia
570	6	2.2	149	21	AAG51582	Arabidopsis thalia	643	6	2.2	180	21	AAI4933	Arabidopsis thalia
571	6	2.2	150	20	AAW97817	Rat myelin oligode	644	6	2.2	180	22	AAI25805	Novel human diagno
572	6	2.2	150	21	AAI15502	Arabidopsis thalia	645	6	2.2	181	19	AAH66010	S. pneumoniae deri
573	6	2.2	151	21	AAH36353	AgfA::PT3#8 amino	646	6	2.2	181	24	ABH1582	Streptococcus pneu
574	6	2.2	151	21	AAH36340	Arabidopsis thalia	647	6	2.2	181	24	ABH1582	S. pneumoniae type
575	6	2.2	151	22	ABH10499	Human cDNA SEQ ID	648	6	2.2	182	22	AAU64222	Propionibacterium
576	6	2.2	151	22	AAU18054	Human immunoglobul	649	6	2.2	185	21	AAO41193	Arabidopsis thalia
577	6	2.2	151	23	ABP67086	Human polypeptide	650	6	2.2	185	21	AAI2732	Arabidopsis thalia
578	6	2.2	152	21	AAH11060	Arabidopsis thalia	651	6	2.2	186	22	AAH05177	Human drug metabol
579	6	2.2	152	21	AAH18585	Arabidopsis thalia	652	6	2.2	186	22	AAH95466	Human protein sequ
580	6	2.2	152	21	AAH48278	Arabidopsis thalia	653	6	2.2	191	22	AAH75439	Human colon cancer
581	6	2.2	152	22	AAH91453	C glutamicum prote	654	6	2.2	193	21	AAH75331	Arabidopsis thalia
582	6	2.2	153	21	AAH54424	Zea mays protein f	655	6	2.2	193	22	AAH90120	C glutamicum prote
583	6	2.2	154	18	AAH55359	H. pylori ORF oligo	656	6	2.2	193	22	AAH79323	Corynebacterium gl
584	6	2.2	154	21	AAH11059	Arabidopsis thalia	657	6	2.2	194	21	AAH53023	Human secreted pro
585	6	2.2	154	21	AAH48277	Arabidopsis thalia	658	6	2.2	194	22	AAH67548	Propionibacterium
586	6	2.2	154	21	AAH58679	Zea mays proteoin f	659	6	2.2	195	23	ABH69269	Human polypeptide
587	6	2.2	155	22	AAH47498	PTPase encoded by	660	6	2.2	195	23	ABH33779	Lactococcus lactis
588	6	2.2	156	21	AAH11058	Arabidopsis thalia	661	6	2.2	196	23	ABH33830	Lactococcus lactis
589	6	2.2	156	21	AAH48276	Arabidopsis thalia	662	6	2.2	198	21	AAH33467	Arabidopsis thalia
590	6	2.2	156	22	AAH24219	Novel human diagno	663	6	2.2	199	21	AAH99660	Human GTPase assoc
591	6	2.2	156	22	AAH57208	Human brain expres	664	6	2.2	202	20	AAH53573	Human gonadotropin
592	6	2.2	156	22	AAH78289	Human bone marrow	665	6	2.2	203	21	AAH54264	Human pancreatic c
593	6	2.2	156	22	AAH17422	Peptide #3856 enco	666	6	2.2	203	22	ABG50590	Human liver peptid

667	6	2.2	203	22	ABB30559	Peptide #3210 enco	740	245	21	AAB43361	Human ORFX ORF3125
668	6	2.2	203	22	ABB35724	Peptide #3230 enco	741	245	21	AAG29538	Arabidopsis thalia
669	6	2.2	203	22	ABB21150	Protein #3149 enco	742	245	22	AAB73692	Human oxidoreducta
670	6	2.2	203	22	AAB65533	Human brain expres	743	245	22	AAB84368	Amino acid sequenc
671	6	2.2	203	22	AAM68915	Human bone marrow	744	245	22	AAG78802	Short-chain dehydr
672	6	2.2	203	22	AAM16738	Peptide #3172 enco	745	245	23	ABP43639	21615 ADH. Homo s
673	6	2.2	203	22	AAM23226	Peptide #3137 enco	746	245	23	ABG34070	Human pro peptide
674	6	2.2	203	22	AAM04455	Peptide #3137 enco	747	245	23	AAU76224	Human 21615 alcoh
675	6	2.2	203	22	ABG38496	Human peptide enco	748	245	23	AAU76224	Actinomadura hibis
676	6	2.2	203	22	ABP41242	Human ovation anti	749	246	21	AAV54386	Human secreted pro
677	6	2.2	203	22	AAU05173	Human expressed pr	750	246	21	AAV54386	Human secreted pro
678	6	2.2	204	22	AAB63960	Human prostate can	751	246	21	AAV54386	Human gastric can
679	6	2.2	206	22	AAB66042	Drosophila melanog	752	247	22	AAG10126	Arabidopsis thalia
680	6	2.2	206	22	AAU91312	Human protein NOVI	753	247	22	ABE68065	Drosophila melanog
681	6	2.2	207	22	AAG82967	S. epidermidis ope	754	248	23	ABP27440	Streptococcus poly
682	6	2.2	209	21	AAG85951	Arabidopsis thalia	755	251	18	AAV34409	Lactobacillus coli p
683	6	2.2	211	19	AAW81141	A Histoplasma capsu	756	251	22	AAV344891	Chlamydia pneumoni
684	6	2.2	211	24	ABU00128	Human novel polype	757	251	22	ABE65238	Putative P. abysssi
685	6	2.2	212	24	ABJ26853	Thymidylate synth	758	252	22	AAB96231	Recombinant mosqui
686	6	2.2	214	22	AAU23332	Novel human enzyme	759	253	19	AAW47358	Aed a 3 CDNA clone
687	6	2.2	214	23	ABB77428	Human tumour marke	760	253	20	AAV17437	Arabidopsis thalia
688	6	2.2	215	21	AAW57361	Arabidopsis thalia	761	253	21	AAW47358	Arabidopsis thalia
689	6	2.2	220	21	AAB21244	MmEPV partial fuso	762	253	21	AAG29143	Drosophila melanog
690	6	2.2	220	22	ABG63373	Drosophila melanog	763	253	22	ABG29537	Arabidopsis thalia
691	6	2.2	220	22	ABG90435	C. glutamicum prote	764	253	22	ABG46081	Arabidopsis thalia
692	6	2.2	220	22	ABG63030	Human polypeptide	765	253	22	AAU34686	Drosophila melanog
693	6	2.2	221	21	ABG63341	Drosophila melanog	766	253	22	AAU34686	E. coli cellular p
694	6	2.2	223	21	AAG29539	Arabidopsis thalia	767	253	22	AAU38285	Salmonella typhi c
695	6	2.2	224	22	AAU81711	Novel central nerv	768	253	22	AAU38285	Propionibacterium
696	6	2.2	224	22	AAU43520	Human polypeptide	769	254	22	AAU32078	Arabidopsis transc
697	6	2.2	224	22	AAU19935	Novel human calciu	770	254	22	AAU32078	Drosophila melanog
698	6	2.2	225	21	AAG14316	Arabidopsis thalia	771	254	22	ABG49981	C. glutamicum SPT
699	6	2.2	225	21	ABG63449	Drosophila melanog	772	254	22	ABG49981	Streptococcus poly
700	6	2.2	226	19	AAW73397	Staphylococcus aur	773	255	21	AAG59509	Arabidopsis thalia
701	6	2.2	230	22	ABE58344	Drosophila melanog	774	255	22	ABG29988	Yeast selected int
702	6	2.2	230	22	AAU54317	Propionibacterium	775	256	23	ABJ10953	Human liver peptid
703	6	2.2	230	22	ABP30530	Streptococcus poly	776	257	22	ABG51845	Drosophila melanog
704	6	2.2	231	23	ABP28562	Streptococcus poly	777	257	22	ABG59275	Drosophila melanog
705	6	2.2	232	21	AAG40276	Arabidopsis thalia	778	257	22	ABG70701	Klebsiella pneumon
706	6	2.2	232	22	ABG58317	Arabidopsis thalia	779	257	22	AAU36113	Propionibacterium
707	6	2.2	235	21	AAW43848	Human cancer assoc	780	257	22	AAU46230	Peptide #4420 enco
708	6	2.2	235	21	AAW45276	Novel human enzyme	781	257	22	ABG31769	Peptide #4501 enco
709	6	2.2	236	21	ABG45276	Protein fragment #	782	257	22	ABG36995	Protein #4309 enco
710	6	2.2	236	21	ABG09577	Novel human diagn	783	257	22	ABG36995	Human brain expres
711	6	2.2	237	23	ABG72187	Human zinc finger	784	257	22	AAW70135	Human bone marrow
712	6	2.2	239	22	AAU7529	Arabidopsis thalia	785	257	22	AAW70135	Peptide #4403 enco
713	6	2.2	239	22	ABG5337	Propionibacterium	786	257	22	AAW70135	Peptide #4510 enco
714	6	2.2	239	22	ABG5337	Human protein sequ	787	257	22	AAW70135	Peptide #4286 enco
715	6	2.2	239	22	ABG5736	Human polypeptide	788	258	21	ABG39774	Human peptide enco
716	6	2.2	239	23	ABG90401	Human RNA metaboli	789	260	21	AAV32318	Arabidopsis thalia
717	6	2.2	239	23	ABE15248	Human RNA metaboli	790	260	23	ABG56534	Human short chain
718	6	2.2	239	23	AAE13229	Arabidopsis thalia	791	261	23	AAE20115	Lactobacillus rham
719	6	2.2	240	21	ABP65279	Bifidobacterium lo	792	262	21	AAE20115	Drosophila thalia
720	6	2.2	240	21	AAU90060	N-terminal sequenc	793	262	22	ABG69111	Streptococcus coli p
721	6	2.2	241	10	AAU90060	Acetoacetyl CoA re	794	263	22	ABG69111	Escherichia coli p
722	6	2.2	241	12	AAU10679	Flagellin excretor	795	263	22	ABG69111	Lactobacillus coli p
723	6	2.2	241	18	AAW26128	Breast and ovarian	796	264	24	ABP60424	Human nucleic acid
724	6	2.2	241	21	AAW58902	Human Blys binding	797	264	24	AAO19611	Human nucleic acid
725	6	2.2	242	21	ABG38843	Arabidopsis thalia	798	265	21	AAO19611	Human nucleic acid
726	6	2.2	242	23	ABP455873	Lactococcus lactis	799	265	21	AAO19611	Arabidopsis thalia
727	6	2.2	242	23	ABP27345	Streptococcus poly	800	265	21	AAO19611	Arabidopsis thalia
728	6	2.2	243	20	AAV48390	Human prostate can	801	265	21	AAO19611	Arabidopsis thalia
729	6	2.2	244	21	AAV54421	Amino acid sequenc	802	266	21	AAO19611	Arabidopsis thalia
730	6	2.2	244	21	AAV54421	Human secreted pro	803	267	21	AAO19611	Human protein clon
731	6	2.2	244	21	AAV54421	E. coli cellular p	804	267	21	AAO19611	Human RECAP polype
732	6	2.2	244	22	AAU34533	Salmonella typhi c	805	267	22	AAO19611	Human secreted pro
733	6	2.2	244	22	AAU34533	Novel human secre	806	267	22	AAO19611	Novel human secre
734	6	2.2	244	22	AAU34533	Human novel cytoki	807	268	22	AAO19611	H. pylori ORF hpa
735	6	2.2	244	22	AAU34533	Human novel cytoki	808	268	22	AAO19611	Bifidobacterium lo
736	6	2.2	244	23	ABU10969	Human short chain	809	269	16	AAU31159	Bifidobacterium lo
737	6	2.2	244	23	ABG65648	Human short chain	810	269	23	ABP65877	Drosophila melanog
738	6	2.2	244	23	ABU01873	S. pneumoniae type	811	270	22	ABG65846	Propionibacterium
739	6	2.2	245	18	AAW55497	H. pylori ORF 01ge	812	271	22	AAU49489	Staphylococcus epi

813	6	2.2	273	10	AAP94155	Acetyl-CoA reducta	886	2.2	302	23	ABB55540	Lactococcus lactis
814	6	2.2	273	12	AAR13141	B.burgdorferi str	887	2.2	304	21	AAAG10125	Arabidopsis thalia
815	6	2.2	273	16	AAR75733	B31/Pgau outer sur	888	2.2	304	21	AAG38842	Arabidopsis thalia
816	6	2.2	273	16	AAR75724	B.burgdorferi str	889	2.2	307	20	AAW83373	Streptococcus pneu
817	6	2.2	273	21	AAG40275	Arabidopsis thalia	890	2.2	307	23	ABP65479	Bifidobacterium lo
818	6	2.2	273	23	AAU79603	Borrelia strain PG	891	2.2	308	21	AAAB42901	Human GRFX ORF265
819	6	2.2	273	23	AAU79612	Borrelia OspA-B31/	892	2.2	308	21	AAG35504	Arabidopsis thalia
820	6	2.2	273	23	AAU91490	Outer surface prot	893	2.2	309	22	AAG71525	Human olfactory re
821	6	2.2	273	23	AAU91493	Outer surface prot	894	2.2	309	23	ABJ04029	Human G-protein co
822	6	2.2	274	22	AAU18491	Human polypeptide	895	2.2	309	23	ABB90219	Human polypeptide
823	6	2.2	274	23	AAO22161	Ramoplanin biosynt	896	2.2	309	23	ABBS3928	Lactococcus lactis
824	6	2.2	275	21	ABG15500	Arabidopsis thalia	897	2.2	310	22	AAU35114	Enterococcus faeca
825	6	2.2	275	22	ABB60233	Drosophila melanog	898	2.2	311	23	ABP60861	Helicobacter pylor
826	6	2.2	275	22	ABG2468	Human protein sequ	899	2.2	311	23	ABP60862	Helicobacter pylor
827	6	2.2	275	23	ABB93346	Herbicidally activ	900	2.2	312	23	ABP51656	Human MAP kinase p
828	6	2.2	276	22	AAU19523	Human diagnostic a	901	2.2	313	23	ABP64798	Human protein SEQ
829	6	2.2	276	22	ABP28780	Streptococcus poly	902	2.2	313	23	ABBS3515	Lactococcus lactis
830	6	2.2	277	21	AAG04192	Arabidopsis thalia	903	2.2	314	20	AAW88347	Salmonella enteric
831	6	2.2	277	21	AAG12731	Arabidopsis thalia	904	2.2	314	22	AAB83955	Amino acid sequenc
832	6	2.2	277	23	ABB93346	Herbicidally activ	905	2.2	314	23	ABB94333	Chlamydia pneumoni
833	6	2.2	278	21	AAU96729	PRO1800. a Hep27 h	906	2.2	315	17	AAR89323	Rape leaf beta-ket
834	6	2.2	278	21	AAU68735	Short chain alcoho	907	2.2	315	17	AAR89322	Rape seed beta-ket
835	6	2.2	278	22	AAB93414	Human protein sequ	908	2.2	315	19	AAW61616	Clone HMCR70 of I
836	6	2.2	278	23	ABG31395	Human PRO1800 poly	909	2.2	315	21	ABG36461	Arabidopsis thalia
837	6	2.2	278	23	ABG91355	Novel human secret	910	2.2	315	23	ABP60866	Mycoplasma pneumon
838	6	2.2	278	23	ABG92703	Human secreted pro	911	2.2	316	23	ABP65646	Bifidobacterium lo
839	6	2.2	278	23	AAU86157	Human PRO1800 poly	912	2.2	316	23	ABG66824	Human prostate spe
840	6	2.2	278	24	ABU60807	Human secreted/tra	913	2.2	317	21	AAG08874	Arabidopsis thalia
841	6	2.2	278	24	ABG73308	Human PRO1800 poly	914	2.2	317	21	AAG09200	Arabidopsis thalia
842	6	2.2	279	22	AAG90188	C glutamicum prote	915	2.2	317	23	AAE22736	MAP kinase phosphat
843	6	2.2	280	21	AAG14532	Arabidopsis thalia	916	2.2	318	18	AAW18337	Murine liver p32 1
844	6	2.2	280	22	ABBS8639	Drosophila melanog	917	2.2	318	20	AAU02004	A retinol dehydrog
845	6	2.2	280	22	AAU93983	Human protein sequ	918	2.2	319	21	AAU10905	S. aureus hydroxic
846	6	2.2	281	23	ABBS3574	Lactococcus lactis	919	2.2	319	21	AAU10124	Arabidopsis thalia
847	6	2.2	282	21	AAU91301	Group B Streptococ	920	2.2	320	22	AAU60254	Propionibacterium
848	6	2.2	282	23	ABP73909	Candida albicans e	921	2.2	320	22	AAU78980	C. glutamicum SRT
849	6	2.2	283	22	ABG62175	Drosophila melanog	922	2.2	320	23	ABU49122	Listeria monocytog
850	6	2.2	284	22	ABU66010	Drosophila melanog	923	2.2	321	21	AAG28323	Arabidopsis thalia
851	6	2.2	284	22	AAU67996	Propionibacterium	924	2.2	322	20	AAU74098	Human prostate tum
852	6	2.2	286	22	AAU34096	Staphylococcus aur	925	2.2	322	21	ABG36460	Arabidopsis thalia
853	6	2.2	286	22	AAU7080	Staphylococcus aur	926	2.2	322	23	ABP69845	Human polypeptide
854	6	2.2	287	14	AAR35435	Staphylococcus aur	927	2.2	323	22	AAU35884	Helicobacter pylor
855	6	2.2	287	22	AAG74298	B. burgdorferi str	928	2.2	323	22	AAU00481	S. galli laevis dTDP
856	6	2.2	287	22	AAG81687	Human colon cancer	929	2.2	323	23	ABU52037	Helicobacter pylor
857	6	2.2	288	9	AAP20501	S. epidermidis ope	930	2.2	325	20	AAU02465	Polyepitide isolat
858	6	2.2	288	20	AAU29081	Cl-inhibitor. Uni	931	2.2	325	22	AAU24632	Human olfactory re
859	6	2.2	288	20	AAU29082	T. gondii immunoge	932	2.2	325	22	AAU24632	Corynebacterium gl
860	6	2.2	288	22	AAU29552	T. gondii immunoge	933	2.2	325	23	ABP95749	Human GPCR polypep
861	6	2.2	288	22	AAU29553	T. gondii immunoge	934	2.2	325	23	AAU95611	Human olfactory an
862	6	2.2	290	22	ABBS2563	Escherichia coli p	935	2.2	325	23	AAU85252	G-coupled olfactor
863	6	2.2	290	24	ABP78330	N. gonorrhoeae ami	936	2.2	325	24	ABP72220	Human G-protein co
864	6	2.2	292	21	AAU96266	K. aestuarii carbo	937	2.2	326	18	AAW21022	H. pylori cytoplas
865	6	2.2	292	22	AAG92082	C glutamicum prote	938	2.2	326	21	AAU70153	Staphylococcus aur
866	6	2.2	293	22	AAU36606	Staphylococcus aur	939	2.2	326	22	ABG64046	Drosophila melanog
867	6	2.2	293	22	ABG82270	S. epidermidis ope	940	2.2	326	23	AAE25702	Staphylococcus aur
868	6	2.2	294	22	ABG69041	Drosophila melanog	941	2.2	327	21	AAU43417	Human cancer assoc
869	6	2.2	294	23	ABU49569	Actinoplanes sp ac	942	2.2	327	21	AAG09199	Arabidopsis thalia
870	6	2.2	294	23	ABU49566	Listeria monocytog	943	2.2	328	21	AAG08873	Arabidopsis thalia
871	6	2.2	294	24	ABU25625	Aspergillus fumiga	944	2.2	328	21	AAU52389	Human transmembran
872	6	2.2	295	22	AAU36240	Pseudomonas aerugi	945	2.2	329	23	ABP28231	Streptococcus poly
873	6	2.2	295	22	AAU79400	Corynebacterium gl	946	2.2	330	18	AAW20625	H. pylori cytoplas
874	6	2.2	295	22	AAU79401	Corynebacterium gl	947	2.2	330	22	AAU36613	Human FLEXHT-35 pr
875	6	2.2	295	23	ABP39214	Staphylococcus epi	948	2.2	331	19	AAW48748	Human granulocytic
876	6	2.2	296	20	AAU23799	A gyrase protein s	949	2.2	331	23	ABU49260	Listeria monocytog
877	6	2.2	296	20	AAU34800	Chlamydia pneumoni	950	2.2	332	20	AAU42333	Staphylococcus aur
878	6	2.2	296	21	AAU96270	K. aestuarii carbo	951	2.2	332	20	AAU31826	Staphylococcus aur
879	6	2.2	296	22	AAG92779	C glutamicum prote	952	2.2	332	22	AAU39371	Human polypeptide
880	6	2.2	296	22	AAG81281	Human APP protein	953	2.2	332	22	AAU41157	Human polypeptide
881	6	2.2	297	22	AAU23504	Novel human enzyme	954	2.2	332	22	AAG93303	Human protein HP10
882	6	2.2	297	22	AAU17597	Novel signal trans	955	2.2	332	22	ABU94250	Human protein sequ
883	6	2.2	298	22	AAG82115	S. epidermidis ope	956	2.2	332	22	ABU94873	Human protein sequ
884	6	2.2	300	23	ABU48784	Listeria monocytog	957	2.2	332	23	AAU15246	Human RNA metaboli
885	6	2.2	301	21	AAG59508	Arabidopsis thalia	958	2.2	333	22	AAU30724	Novel human secret

959 6 2.2 333 22 AAB59871 Phosphotransacetyl  
960 6 2.2 335 22 AAU16225 Human novel secret  
961 6 2.2 335 24 ABUS5294 Human novel polype  
962 6 2.2 336 16 AAW06488 Maize Ts2 sequence  
963 6 2.2 336 20 AAY41730 Human PRO1073 prot  
964 6 2.2 336 21 AAB41286 Human PRO1072 (UNQ  
965 6 2.2 336 22 AAU23114 Human PRO polypept  
966 6 2.2 336 22 AAE02575 Enterococcus crypt  
967 6 2.2 336 23 ABUS1350 Helicobacter pylor  
968 6 2.2 336 24 ABU71202 Human PRO1072 prot  
969 6 2.2 336 24 ABUS6569 Human secreted/tra  
970 6 2.2 336 24 ABUS6592 Human secreted/tra  
971 6 2.2 336 24 ABUS67496 Human secreted/tra  
972 6 2.2 336 24 ABUS61116 Human PRO1072 poly  
973 6 2.2 336 24 ABUS63354 Human PRO polypept  
974 6 2.2 336 24 ABUS58490 Human PRO polypept  
975 6 2.2 336 24 ABUS56026 Human secreted/tra  
976 6 2.2 336 24 ABUS7021 Human PRO polypept  
977 6 2.2 336 24 ABU10600 Human secreted/tra  
978 6 2.2 338 14 AAR33449 NS1-ACAI fusion pr  
979 6 2.2 338 14 AAR32282 Mouse FosB2. Mus  
980 6 2.2 338 21 AAY58001 Saccharomyces cere  
981 6 2.2 338 21 ABB57357 Mouse ischaemic co  
982 6 2.2 338 23 AAG66011 Amino acid sequenc  
983 6 2.2 341 20 AAY30883 Human secreted pro  
984 6 2.2 342 20 AAY05771 Saccharomyces cere  
985 6 2.2 342 22 AAG18424 Novel human diagno  
986 6 2.2 342 22 AAG63567 Amino acid sequenc  
987 6 2.2 342 23 AAG51011 Helicobacter pylor  
988 6 2.2 342 23 ABB93197 S. cerevisiae BAX-  
989 6 2.2 342 23 ABB93772 Herbicidally activ  
990 6 2.2 342 22 AAG63568 Synthetic amino ac  
991 6 2.2 345 11 AAR02218 Sequence encoding  
992 6 2.2 345 11 AAR02218 Influenza type B H  
993 6 2.2 345 15 AAR51848 Influenza type B H  
994 6 2.2 345 15 AAR51849 Influenza type B H  
995 6 2.2 345 15 AAR51850 Influenza type B H  
996 6 2.2 345 15 AAR51851 Influenza type B H  
997 6 2.2 345 15 AAR51852 Influenza type B H  
998 6 2.2 345 15 AAR51853 Influenza type B H  
999 6 2.2 345 15 AAR51854 Influenza type B H  
1000 6 2.2 345 15 AAR51855 Influenza type B H

ALIGNMENTS

RESULT 1  
ID AAY54412 standard; Protein; 273 AA.  
AC AAY54412;  
DT 06-APR-2000 (first entry)  
DE Secoisolariciresinol dehydrogenase protein clone DEHY133.  
KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
OS Forsythia intermedia.  
PN WO955846-A1.  
PD 04-NOV-1999.  
PF 23-APR-1999; 99WO-US08975.  
PR 24-APR-1998; 98US-0082977.  
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Xia Z, Costa MA, Davin LB, Lewis NG;  
PI WPI: 2000-126356/11.  
XX N-PSDB; AA245730.  
DR New nucleic acid molecule encoding an enzyme involved in lignan  
XX biosynthetic pathway, useful for producing large amounts of lignans -  
PT Claim 8; Page 46-47; 66pp; English.  
XX The present sequence represents a secoisolariciresinol dehydrogenase  
CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
CC The secoisolariciresinol dehydrogenase proteins have a molecular  
CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
CC nucleic acids are used for the recombinant expression of the enzymes.  
CC It is also used to obtain expression or enhanced expression of  
CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
CC biosynthesis. The enzyme is used for production of the pharmacologically  
CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
CC proteins and nucleic acids can be utilized to: elevate or otherwise  
CC alter the levels of health-protecting lignans, including phytoestrogens  
CC such as enterolactone and enterodiol, in plant species, including  
CC vegetables, grains and fruits and to food items incorporating material  
CC derived from such genetically altered plants; genetically alter plant  
CC species to provide an abundant, natural supply of lignans useful for  
CC a variety of purposes, for example as neutriceuticals and dietary  
CC supplements; to genetically alter living organisms to produce an  
CC abundant supply of optically pure lignans having desirable biological  
CC properties, for example (-)-trachelogenin which possesses antiviral  
CC properties, and (-)-podophyllotoxin.  
XX SQ Sequence 273 AA;  
Query Match 100.0%; Score 273; DB 21; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1.5e-270;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQLRTAFARLRGKVALITGASGIGETTAKLFQSHGAKVAIADVDQDELGSHVVEAIGTS 60  
DB 1 MQLRTAFARLRGKVALITGASGIGETTAKLFQSHGAKVAIADVDQDELGSHVVEAIGTS 60  
QY 61 NSTYIHCDVTNEDGVKNAVDNTVSTYKGLDIMPNSAGISDPNRPRIIDNEKADFERVLSV 120  
DB 61 NSTYIHCDVTNEDGVKNAVDNTVSTYKGLDIMPNSAGISDPNRPRIIDNEKADFERVLSV 120  
QY 121 NVTGVFLCMKHAARVMIIPARSGNIISTASLSSTWGGSSSHAYCGSHAVLALTRNLAVEL 180  
DB 121 NVTGVFLCMKHAARVMIIPARSGNIISTASLSSTWGGSSSHAYCGSHAVLALTRNLAVEL 180  
QY 181 GQFGIRVNCISDPGLPTALGKKEEFENFVINFAGNLKPKFKNVEDVANALYLA 240  
DB 181 GQFGIRVNCISDPGLPTALGKKEEFENFVINFAGNLKPKFKNVEDVANALYLA 240  
QY 241 SDEAKYVSGHNLFDGFGFSVCNSVIKVFQYDPS 273  
DB 241 SDEAKYVSGHNLFDGFGFSVCNSVIKVFQYDPS 273  
RESULT 2  
ID AAY54420 standard; Protein; 272 AA.  
AC AAY54420;  
XX AAY54420;  
DT 06-APR-2000 (first entry)  
DE Secoisolariciresinol dehydrogenase protein clone DEHY130.  
KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

OS Forsythia intermedia.

XX WO9955846-A1.

XX 04-NOV-1999.

XX 23-APR-1999; 99WO-US089975.

XX 24-APR-1998; 98US-0082977.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Xia Z, Costa MA, Davin LB, Lewis NG;

XX WPI; 2000-126356/11.

XX N-PSDB; AAZ45743.

XX New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans

XX Example 2; Page 61-63; 66pp; English.

XX The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise alter the levels of health-protecting lignans, including phytoestrogens such as enterolactone and enterodiol, in plant species, including vegetables, grains and fruits and to food items incorporating material derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as nutraceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, for example (-)-trachelogenin which possesses antiviral properties, and (-)-podophyllotoxin.

XX Sequence 272 AA;

Query Match 99.6%; Score 272; DB 21; Length 272;

Best Local Similarity 100.0%; Pred. No. 1.6e-269;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QLRFAFARLEKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHVWEAIGTSN 61

Db 1 QLRFAFARLEKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHVWEAIGTSN 60

Qy 62 STYIHCVDVTNEDGVKNVNTVSTYGLDIFMFSNAGISDPNRPRIIDNEKADFERVLSVN 121

Db 61 STYIHCVDVTNEDGVKNVNTVSTYGLDIFMFSNAGISDPNRPRIIDNEKADFERVLSVN 120

Qy 122 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVAVALTRNLAVELG 181

Db 121 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVAVALTRNLAVELG 180

Qy 182 QFGIRVNCCLSPFGLPTALGKFKFSIGKNEEPEENVINFAGNLKGPKNVEDVANAALYLAS 241

Db 181 QFGIRVNCCLSPFGLPTALGKFKFSIGKNEEPEENVINFAGNLKGPKNVEDVANAALYLAS 240

Qy 242 DEAKVVSGHNLFIDGGFSCVNCNVKVFQYRPS 273

Db 241 DEAKVVSGHNLFIDGGFSCVNCNVKVFQYRPS 272

RESULT 3

AAAY54413

ID AAY54413 standard; Protein; 277 AA.

XX AC AAY54413;

XX DT 06-APR-2000 (first entry)

XX DE Secoisolariciresinol dehydrogenase protein clone SMDBHY321.

XX KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;

XX KW lignan; matairesinol; health-protecting lignan; phytoestrogen;

XX KW enterolactone; enterodiol; nutraceutical; dietary supplement;

XX KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

XX OS Forsythia intermedia.

XX PN WO9955846-A1.

XX PD 04-NOV-1999.

XX PF 23-APR-1999; 99WO-US089975.

XX PR 24-APR-1998; 98US-0082977.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Xia Z, Costa MA, Davin LB, Lewis NG;

XX WPI; 2000-126356/11.

XX DR N-PSDB; AAZ45731.

XX PT New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans

XX PS Claim 8; Page 49-50; 66pp; English.

XX The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise alter the levels of health-protecting lignans, including phytoestrogens such as enterolactone and enterodiol, in plant species, including vegetables, grains and fruits and to food items incorporating material derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as nutraceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, for example (-)-trachelogenin which possesses antiviral properties, and (-)-podophyllotoxin.

XX Sequence 277 AA;

Query Match 40.3%; Score 110; DB 21; Length 277;

Best Local Similarity 100.0%; Pred. No. 7.9e-104;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ARRLGKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHVWEAIGTSNVIHC 67

Db 12 ARRLGKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHVWEAIGTSNVIHC 71

Qy 68 DVTNEDGVKNVNTVSTYGLDIFMFSNAGISDPNRPRIIDNEKADFERV 117

Db 72 DVTNEDGVKNVNTVSTYGLDIFMFSNAGISDPNRPRIIDNEKADFERV 121

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RESULT 4
AAV5414
ID AAY54414 standard; Protein; 273 AA.
AC AAY54414;
XX
DT 06-APR-2000 (first entry)
XX
DE Secoisolaricresinol dehydrogenase protein clone SMDEHY431.
XX
KW Secoisolaricresinol dehydrogenase; lignan biosynthetic pathway;
KW lignan; metairesinol; health-protecting lignan; phytoestrogen;
KW enterolactone; enterodiol; neutraceutical; dietary supplement;
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
XX
OS Forsythia intermedia.
XX
FH Key Location/Qualifiers
FT Misc-difference 120
FT /notes "encoded by GTN"
FT Misc-difference 122
FT /notes "encoded by GTN"
XX
PN WO9955846-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US089975.
XX
PR 24-APR-1998; 98US-0082977.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Xia Z, Costa MA, Davin LB, Lewis NG;
XX
DR WPI; 2000-126356/11.
XX
DR N-PSDB; AAZ45734.
XX
PT New nucleic acid molecule encoding an enzyme involved in lignan
PT biosynthetic pathway, useful for producing large amounts of lignans
PS Claim 8; Page 51-52; 66pp; English.
XX
XX
XX The present sequence represents a secoisolaricresinol dehydrogenase
XX protein. The enzyme is involved in the lignan biosynthetic pathway.
XX The secoisolaricresinol dehydrogenase proteins have a molecular
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require
XX NAD or NADP as a cofactor. The secoisolaricresinol dehydrogenase
XX nucleic acids are used for the recombinant expression of the enzymes.
XX It is also used to obtain expression or enhanced expression of
XX secoisolaricresinol dehydrogenase in plants or to alter lignan
XX biosynthesis. The enzyme is used for production of the pharmacologically
XX active lignan, metairesinol. The secoisolaricresinol dehydrogenase
XX proteins and nucleic acids can be utilized to: elevate or otherwise
XX alter the levels of health-protecting lignans, including phytoestrogens
XX such as enterolactone and enterodiol, in plant species, including
XX vegetables, grains and fruits and to food items incorporating material
XX derived from such genetically altered plants; genetically alter plant
XX species to provide an abundant, natural supply of lignans useful for
XX a variety of purposes, for example as nutraceuticals and dietary
XX supplements; to genetically alter living organisms to produce an
XX abundant supply of optically pure lignans having desirable biological
XX properties, for example (-)-trachelogenin which possesses antiviral
XX properties, and (-)-podophyllotoxin.
XX
XX Sequence 273 AA;
XX
Query Match 12.5%; Score 34; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
80
60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93

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|||||
Db 60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93
|||||
RESULT 5
AAV5416
ID AAY54416 standard; Protein; 276 AA.
AC AAY54416;
XX
DT 06-APR-2000 (first entry)
XX
DE Secoisolaricresinol dehydrogenase protein clone SMDEHY631.
XX
KW Secoisolaricresinol dehydrogenase; lignan biosynthetic pathway;
KW lignan; metairesinol; health-protecting lignan; phytoestrogen;
KW enterolactone; enterodiol; neutraceutical; dietary supplement;
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
XX
OS Forsythia intermedia.
XX
PN WO9955846-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US089975.
XX
PR 24-APR-1998; 98US-0082977.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Xia Z, Costa MA, Davin LB, Lewis NG;
XX
DR WPI; 2000-126356/11.
XX
DR N-PSDB; AAZ45734.
XX
PT New nucleic acid molecule encoding an enzyme involved in lignan
PT biosynthetic pathway, useful for producing large amounts of lignans
PS Claim 8; Page 56-57; 66pp; English.
XX
XX
XX The present sequence represents a secoisolaricresinol dehydrogenase
XX protein. The enzyme is involved in the lignan biosynthetic pathway.
XX The secoisolaricresinol dehydrogenase proteins have a molecular
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require
XX NAD or NADP as a cofactor. The secoisolaricresinol dehydrogenase
XX nucleic acids are used for the recombinant expression of the enzymes.
XX It is also used to obtain expression or enhanced expression of
XX secoisolaricresinol dehydrogenase in plants or to alter lignan
XX biosynthesis. The enzyme is used for production of the pharmacologically
XX active lignan, metairesinol. The secoisolaricresinol dehydrogenase
XX proteins and nucleic acids can be utilized to: elevate or otherwise
XX alter the levels of health-protecting lignans, including phytoestrogens
XX such as enterolactone and enterodiol, in plant species, including
XX vegetables, grains and fruits and to food items incorporating material
XX derived from such genetically altered plants; genetically alter plant
XX species to provide an abundant, natural supply of lignans useful for
XX a variety of purposes, for example as nutraceuticals and dietary
XX supplements; to genetically alter living organisms to produce an
XX abundant supply of optically pure lignans having desirable biological
XX properties, for example (-)-trachelogenin which possesses antiviral
XX properties, and (-)-podophyllotoxin.
XX
XX Sequence 276 AA;
XX
Query Match 12.5%; Score 34; DB 21; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
80
60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93
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KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX Forsythia intermedia.  
 XX WO955846-A1.  
 XX 04-NOV-1999.  
 XX 23-APR-1999; 99WO-US08975.  
 XX 24-APR-1998; 98US-0082977.  
 XX (UNIV ) UNIV WASHINGTON STATE RES FOUND.  
 XX Xia Z, Costa MA, Davin LB, Lewis NG;  
 XX WPI; 2000-126356/11.  
 XX New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans -  
 XX Example 1; Page 58; 66pp; English.  
 XX The present sequence represents a peptide of a secoisolariciresinol  
 XX dehydrogenase. The enzyme is involved in the lignan biosynthetic pathway.  
 XX The secoisolariciresinol dehydrogenase proteins have a molecular  
 XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 XX NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 XX nucleic acids are used for the recombinant expression of the enzymes.  
 XX It is also used to obtain expression or enhanced expression of  
 XX secoisolariciresinol dehydrogenase in plants or to alter lignan  
 XX biosynthesis. The enzyme is used for production of the pharmacologically  
 XX active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 XX proteins and nucleic acids can be utilized to: elevate or otherwise  
 XX alter the levels of health-protecting lignans, including phytoestrogens  
 XX such as enterolactone and enterodiol, in plant species, including  
 XX vegetables, grains and fruits and to food items incorporating material  
 XX derived from such genetically altered plants; genetically alter plant  
 XX species to provide an abundant, natural supply of lignans useful for  
 XX a variety of purposes, for example as nutraceuticals and dietary  
 XX supplements; to genetically alter living organisms to produce an  
 XX abundant supply of optically pure lignans having desirable biological  
 XX properties, for example (-)-trachelogenin which possesses antiviral  
 XX properties, and (-)-podophyllotoxin.  
 XX Sequence 17 AA;  
 XX  
 XX Query Match 6.2%; Score 17; DB 21; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 7.6e-10;  
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 VALITGASGIGTTAK 31  
 Db 1 VALITGASGIGTTAK 17  
 RESULT 9  
 ID AAG31552  
 XX AAG31552 standard; Protein; 283 AA.  
 AC AAG31552;  
 XX 17-OCT-2000 (first entry)  
 DT Arabidopsis thaliana protein fragment SEQ ID NO: 37910.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 37910.  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX EP1033405-A2.  
 XX  
 XX 06-SEP-2000.  
 XX 25-FEB-2000; 2000EP-0301439.  
 XX 25-FEB-1999; 99US-0121825.  
 XX 05-MAR-1999; 99US-0123180.  
 XX 23-MAR-1999; 99US-0123548.  
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 XX 06-MAY-1999; 99US-0132484.  
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 XX 24-JUN-1999; 99US-0140354.  
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 XX 01-JUL-1999; 99US-0141542.  
 XX 01-JUL-1999; 99US-0142154.  
 XX 01-JUL-1999; 99US-0142154.



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PR 26-AUG-1999; 99US-0150884.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 5.9%; Score 16; DB 21; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.le-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGAGCIG 26  
Db 18 LEGKVALITGAGCIG 33

## RESULT 10

ABB92823  
ID ABB92823 standard; Protein; 283 AA.

XX ABB92823;  
XX AC  
XX

DT 31-MAY-2002 (first entry)

XX Herbicidally active polypeptide SEQ ID NO 2034.

DE Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP09892.

XX 28-AUG-2001; 2001WO-EP09892.

XX (FARB ) BAYER AG.

XX

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PI Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
XX
XX Identifying plant target proteins for herbicidally active compounds,
XX comprising aligning and comparing nucleic acid or amino acid sequences
XX from plant with nucleic acid or amino acid sequences from non-plant
XX organisms -
XX
XX Claim 5; SEQ ID NO 2034; 261pp + Sequence Listing; English.
XX
XX The invention relates to identifying target proteins
XX (AB90790-AB94016) for herbicidally active compounds, comprising
XX aligning and comparing nucleic acid or amino acid sequences from plant
XX with nucleic acid or amino acid sequences from non-plant organisms using
XX suitable search parameters, where plant sequences having an E-value
XX greater by a factor of 3 than the E-value of most similar non-plant
XX sequences are selected. The polypeptides or nucleic acids encoding them
XX are useful for identifying modulators. The identified modulators are
XX useful as herbicides.
XX
XX Sequence 283 AA;
SQ
Query Match 5.9%; Score 16; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.le-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 18 LEGKVALITGGASGIG 33
RESULT 11
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ID AAG18620 standard; Protein; 300 AA.
XX
XX AAG18620;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 20101.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
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PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      5.9%; Score 16; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 LEGRVALITGGASGIG 26
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DB      35 LEGRVALITGGASGIG 50

RESULT 12
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AC AAG18619;
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DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20100.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Db 78 LEGKVALITGGASGIG 93

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ABB92449  
ID ABB92449 standard; Protein; 280 AA.

XX AC ABB92449;

DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 1660.

XX KW Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

XX PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP09892.

XX PR 28-AUG-2001; 2001WO-EP09892.

XX PA (FARB ) BAYER AG.

XX PI Tietjen K, Weidler M;

XX DR WPI; 2002-269010/31.

XX PT Identifying plant target proteins for herbicidally active compounds,  
XX PT comprising aligning and comparing nucleic acid or amino acid sequences  
XX PT from plant with nucleic acid or amino acid sequences from non-plant  
XX PT organisms -

XX PS Claim 5; SEQ ID NO 1660; 261pp + Sequence Listing; English.

XX CC The invention relates to identifying target proteins  
XX CC (ABB90790-ABB94016) for herbicidally active compounds, comprising  
XX CC aligning and comparing nucleic acid or amino acid sequences from plant  
XX CC with nucleic acid or amino acid sequences from non-plant organisms using  
XX CC suitable search parameters, where plant sequences having an E-value  
XX CC greater by a factor of 3 than the E-value of most similar non-plant  
XX CC sequences are selected. The polypeptides or nucleic acids encoding them  
XX CC are useful for identifying modulators. The identified modulators are  
XX CC useful as herbicides.

XX SQ Sequence 280 AA;

Query Match 5.1%; Score 14; DB 23; Length 280;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
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Qy 11 LEGKVALITGGASG 24

Db 15 LEGKVALITGGASG 28

RESULT 14  
AAV54419  
ID AAV54419 standard; Peptide; 15 AA.

XX AC AAV54419;

XX DT 06-APR-2000 (first entry)

XX DE Trypsin fragment of a secoisolariciresinol dehydrogenase protein.  
XX KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
XX KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
XX KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
XX KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

XX OS Forsythia intermedia.

XX PN WO9955846-A1.

XX PD 04-NOV-1999.

XX PF 23-APR-1999; 99WO-US08975.

XX PR 24-APR-1998; 98US-0082977.

XX PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX PI Xia Z, Costa MA, Davin LB, Lewis NG;

XX DR WPI; 2000-126356/11.

XX PT New nucleic acid molecule encoding an enzyme involved in lignan  
XX PT biosynthetic pathway, useful for producing large amounts of lignans  
XX PS Example 1; Page 58; 66pp; English.

XX CC The present sequence represents a peptide of a secoisolariciresinol  
XX CC dehydrogenase. The enzyme is involved in the lignan biosynthetic pathway.  
XX CC The secoisolariciresinol dehydrogenase proteins have a molecular  
XX CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
XX CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
XX CC nucleic acids are used for the recombinant expression of the enzymes.  
XX CC It is also used to obtain expression or enhanced expression of  
XX CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
XX CC biosynthesis. The enzyme is used for production of the pharmacologically  
XX CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
XX CC proteins and nucleic acids can be utilized to: elevate or otherwise  
XX CC alter the levels of health-protecting lignans, including phytoestrogens  
XX CC such as enterolactone and enterodiol, in plant species, including  
XX CC vegetables, grains and fruits and to food items incorporating material  
XX CC derived from such genetically altered plants; genetically alter plant  
XX CC species to provide an abundant, natural supply of lignans useful for  
XX CC a variety of purposes, for example as neutraceuticals and dietary  
XX CC supplements; to genetically alter living organisms to produce an  
XX CC abundant supply of optically pure lignans having desirable biological  
XX CC properties, for example (-)-trachelogenin which possesses antiviral  
XX CC properties, and (-)-podophyllotoxin.

XX SQ Sequence 15 AA;

Query Match 4.4%; Score 12; DB 21; Length 15;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 IMFSNAGISDPN 102

Db 3 IMFSNAGISDPN 14

RESULT 15  
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ID ABP00547 standard; Protein; 127 AA.

XX AC ABP00547;  
 XX DT 25-JUN-2002 (first entry)  
 XX DE Human ORFX protein sequence SEQ ID NO:1076.  
 XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.  
 XX OS Homo sapiens.  
 XX PN WO200192523-A2.  
 XX PD 06-DEC-2001.  
 XX PF 29-MAY-2001; 2001WO-US10836.  
 XX PR 30-MAY-2000; 2000US-206132P.  
 XX PR 29-AUG-2000; 2000US-228716P.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Shimkets RA, Leach MD;  
 DR WPI: 2002-106308/14.  
 DR N-PSDB; AEN16299.  
 XX PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders  
 XX PS Disclosure; SEQ ID 1076; 1037pp; English.  
 XX CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). AEN15762 to AEN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 127 AA;

Query Match 4.0%; Score 11; DB 23; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 0.0069;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 99 ANAALYLASDE 109  
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 Job time : 117 secs

GenCore version 5.1.6  
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Run on: October 23, 2003, 13:00:45 ; Search time 29 Seconds  
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Title: US-09-673-918A-2

Perfect score: 273

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	8	2.9	267	4	US-09-252-991A-19626
5	8	2.9	290	4	US-09-134-001C-4339
6	8	2.9	295	3	US-09-026-482B-2
7	8	2.9	323	3	US-08-580-545B-2
8	8	2.9	323	3	US-09-262-653A-2
9	7	2.6	87	4	US-09-328-352-4279
10	7	2.6	172	4	US-09-252-991A-21618
11	7	2.6	175	4	US-09-252-991A-18834
12	7	2.6	251	4	US-09-648-004-20
13	7	2.6	261	3	US-08-815-225-2
14	7	2.6	261	3	US-08-815-225-3
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23	7	2.6	340	4	US-09-252-991A-24822
24	7	2.6	370	4	US-09-328-352-5285
25	7	2.6	401	4	US-09-252-991A-19274
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76	6	2.2	126	1	US-08-075-545-2	Sequence 2, Appli
77	6	2.2	127	1	US-08-256-261-8	Sequence 8, Appli
78	6	2.2	127	3	US-08-852-299-8	Sequence 8, Appli
79	6	2.2	128	2	US-08-799-464A-26	Sequence 26, Appl
80	6	2.2	128	4	US-09-331-924-1	Sequence 1, Appli
81	6	2.2	128	5	PCT-US95-09927-26	Sequence 26, Appl
82	6	2.2	128	5	PCT-US95-10904-26	Sequence 26, Appl
83	6	2.2	131	2	US-08-477-451-30	Sequence 30, Appl
84	6	2.2	136	1	US-08-371-505-2	Sequence 2, Appli
85	6	2.2	136	2	US-08-784-371-5	Sequence 5, Appli
86	6	2.2	136	4	US-09-020-018-10	Sequence 10, Appl
87	6	2.2	136	4	US-09-252-991A-21678	Sequence 21678, A
88	6	2.2	137	1	US-08-256-261-2	Sequence 2, Appli
89	6	2.2	137	1	US-08-256-261-4	Sequence 4, Appli
90	6	2.2	137	1	US-08-256-261-6	Sequence 6, Appli
91	6	2.2	137	1	US-08-256-261-12	Sequence 12, Appl
92	6	2.2	137	1	US-08-256-261-14	Sequence 14, Appl
93	6	2.2	137	2	US-08-630-822A-64	Sequence 64, Appl
94	6	2.2	137	2	US-09-005-069-64	Sequence 64, Appl
95	6	2.2	137	3	US-08-852-299-2	Sequence 2, Appli
96	6	2.2	137	3	US-08-852-299-4	Sequence 4, Appli
97	6	2.2	137	3	US-08-852-299-6	Sequence 6, Appli
98	6	2.2	137	3	US-08-852-299-12	Sequence 12, Appl
99	6	2.2	137	3	US-08-852-299-14	Sequence 14, Appl
100	6	2.2	137	4	US-09-171-156A-23	Sequence 23, Appl

101	6	2.2	137	4	US-09-004-730A-23	Sequence 23, Appl	174	6	2.2	222	4	US-09-940-037A-2	Sequence 2, Appl
102	6	2.2	137	4	US-08-981-799A-23	Sequence 23, Appl	175	6	2.2	222	4	US-09-252-991A-28482	Sequence 28482, A
103	6	2.2	138	1	US-08-053-171-7	Sequence 7, Appl	176	6	2.2	224	4	US-09-328-352-6415	Sequence 6415, Ap
104	6	2.2	138	1	US-08-053-171-11	Sequence 11, Appl	177	6	2.2	235	4	US-09-134-001C-4059	Sequence 4059, Ap
105	6	2.2	139	1	US-08-120-607A-11	Sequence 11, Appl	178	6	2.2	236	4	US-09-468-738A-23	Sequence 23, Appl
106	6	2.2	140	1	US-09-904-615-76	Sequence 76, Appl	179	6	2.2	236	4	US-09-940-019-23	Sequence 23, Appl
107	6	2.2	140	1	US-09-107-532A-4251	Sequence 4251, Ap	180	6	2.2	236	4	US-09-940-037A-23	Sequence 23, Appl
108	6	2.2	143	4	US-09-107-532A-4251	Sequence 4251, Ap	181	6	2.2	236	4	US-09-198-452A-218	Sequence 218, App
109	6	2.2	145	4	US-09-733-210-1561	Sequence 1561, Ap	182	6	2.2	304	4	US-09-252-991A-18282	Sequence 18282, A
110	6	2.2	145	6	5338678-210-1593	Sequence 1593, Ap	183	6	2.2	310	4	US-09-252-991A-23088	Sequence 23088, A
111	6	2.2	155	6	5338678-2	Patent No. 5338678	184	6	2.2	314	4	US-09-087-031E-4	Sequence 4, Appl
112	6	2.2	162	4	US-09-006-428A-4	Sequence 4, Appl	185	6	2.2	314	4	US-09-087-031E-4	Sequence 4, Appl
113	6	2.2	163	1	US-08-075-545-1	Sequence 1, Appl	186	6	2.2	314	4	US-09-252-991A-31368	Sequence 31368, A
114	6	2.2	163	1	US-08-258-261-17	Sequence 17, Appl	187	6	2.2	315	3	US-08-793-035-9	Sequence 9, Appl
115	6	2.2	163	3	US-08-852-289-17	Sequence 17, Appl	188	6	2.2	315	3	US-08-793-035-10	Sequence 10, Appl
116	6	2.2	164	3	US-08-728-416C-3	Sequence 3, Appl	189	6	2.2	318	3	US-08-729-594A-39	Sequence 39, Appl
117	6	2.2	164	3	US-08-728-416C-13	Sequence 13, Appl	190	6	2.2	318	3	US-08-937-991-39	Sequence 39, Appl
118	6	2.2	164	4	US-09-433-353-3	Sequence 3, Appl	191	6	2.2	337	4	US-09-252-991A-18869	Sequence 18869, A
119	6	2.2	164	4	US-09-433-353-13	Sequence 13, Appl	192	6	2.2	338	4	US-09-252-991A-31963	Sequence 31963, A
120	6	2.2	164	4	US-09-433-353-21	Sequence 21, Appl	193	6	2.2	339	4	US-09-107-532A-7038	Sequence 7038, Ap
121	6	2.2	171	4	US-09-252-991A-27423	Sequence 27423, A	194	6	2.2	332	4	US-09-830-217-20	Sequence 20, Appl
122	6	2.2	174	4	US-09-252-991A-32138	Sequence 32138, A	195	6	2.2	332	4	US-09-252-991A-21096	Sequence 21096, A
123	6	2.2	176	4	US-09-149-476-440	Sequence 440, App	196	6	2.2	332	4	US-09-252-991A-22834	Sequence 22834, A
124	6	2.2	182	4	US-09-252-991A-17529	Sequence 17529, A	197	6	2.2	332	4	US-09-252-991A-25234	Sequence 25234, A
125	6	2.2	188	4	US-09-252-991A-25186	Sequence 25186, A	198	6	2.2	332	4	US-09-252-991A-26386	Sequence 26386, A
126	6	2.2	202	4	US-09-252-991A-17114	Sequence 17114, A	199	6	2.2	336	3	US-08-855-910-6	Sequence 6, Appl
127	6	2.2	206	4	US-09-328-352-4683	Sequence 4683, Ap	200	6	2.2	337	1	US-08-440-856A-3	Sequence 3, Appl
128	6	2.2	214	4	US-09-252-991A-20677	Sequence 20677, A	201	6	2.2	338	1	US-08-218-686-2	Sequence 2, Appl
129	6	2.2	218	2	US-08-531-525-19	Sequence 19, Appl	202	6	2.2	338	2	US-08-441-857-10	Sequence 10, Appl
130	6	2.2	218	2	US-08-718-270A-19	Sequence 19, Appl	203	6	2.2	338	2	US-09-047-026A-2	Sequence 2, Appl
131	6	2.2	218	4	US-10-026-045-1	Sequence 1, Appl	204	6	2.2	338	3	US-08-460-242-2	Sequence 2, Appl
132	6	2.2	226	4	US-09-252-991A-30546	Sequence 30546, A	205	6	2.2	338	3	US-08-193-159-10	Sequence 10, Appl
133	6	2.2	229	4	US-09-252-991A-29751	Sequence 29751, A	206	6	2.2	339	4	US-09-252-991A-26600	Sequence 26600, A
134	6	2.2	230	4	US-09-252-991A-22090	Sequence 22090, A	207	6	2.2	341	4	US-09-369-247-132	Sequence 132, App
135	6	2.2	232	4	US-09-328-352-8025	Sequence 8025, Ap	208	6	2.2	342	4	US-09-415-277C-8	Sequence 8, Appl
136	6	2.2	236	4	US-09-252-991A-31916	Sequence 31916, A	209	6	2.2	345	1	US-07-954-840A-8	Sequence 8, Appl
137	6	2.2	239	4	US-09-252-991A-26390	Sequence 26390, A	210	6	2.2	345	1	US-07-954-840A-10	Sequence 10, Appl
138	6	2.2	241	4	US-08-178-257-19	Sequence 19, Appl	211	6	2.2	345	1	US-07-954-840A-12	Sequence 12, Appl
139	6	2.2	244	1	US-08-375-962B-13	Sequence 13, Appl	212	6	2.2	345	1	US-07-954-840A-14	Sequence 14, Appl
140	6	2.2	244	3	US-08-562-114B-13	Sequence 13, Appl	213	6	2.2	345	1	US-07-954-840A-16	Sequence 16, Appl
141	6	2.2	244	3	US-08-729-594A-13	Sequence 13, Appl	214	6	2.2	345	1	US-07-954-840A-18	Sequence 18, Appl
142	6	2.2	244	4	US-09-937-991-13	Sequence 13, Appl	215	6	2.2	345	1	US-07-954-840A-20	Sequence 20, Appl
143	6	2.2	246	4	US-09-604-615-13	Sequence 13, Appl	216	6	2.2	345	1	US-07-954-840A-22	Sequence 22, Appl
144	6	2.2	251	3	US-08-822-322-9	Sequence 9, Appl	217	6	2.2	345	1	US-07-954-840A-24	Sequence 24, Appl
145	6	2.2	251	3	US-09-466-109-9	Sequence 9, Appl	218	6	2.2	345	1	US-07-954-840A-26	Sequence 26, Appl
146	6	2.2	251	4	US-09-198-452A-309	Sequence 309, App	219	6	2.2	347	1	US-07-637-870-5	Sequence 5, Appl
147	6	2.2	259	4	US-09-252-991A-28945	Sequence 28945, A	220	6	2.2	347	1	US-07-954-840A-2	Sequence 2, Appl
148	6	2.2	260	3	US-08-729-416C-21	Sequence 21, Appl	221	6	2.2	347	1	US-07-954-840A-4	Sequence 4, Appl
149	6	2.2	260	3	US-08-729-416C-22	Sequence 22, Appl	222	6	2.2	347	1	US-07-954-840A-6	Sequence 6, Appl
150	6	2.2	261	4	US-09-252-991A-17349	Sequence 17349, A	223	6	2.2	347	1	US-07-954-840A-28	Sequence 28, Appl
151	6	2.2	261	4	US-09-252-991A-28346	Sequence 28346, A	224	6	2.2	347	1	US-07-954-840A-29	Sequence 29, Appl
152	6	2.2	263	6	5229279-4	Patent No. 5229279	225	6	2.2	347	1	US-07-640-476-10	Sequence 10, Appl
153	6	2.2	267	4	US-09-328-352-6630	Sequence 6630, Ap	226	6	2.2	347	1	US-09-415-277C-11	Sequence 11, Appl
154	6	2.2	272	4	US-09-134-001C-2864	Sequence 2864, Ap	227	6	2.2	347	4	US-07-637-399-8	Sequence 8, Appl
155	6	2.2	272	4	US-09-328-352-7904	Sequence 7904, Ap	228	6	2.2	348	1	US-08-112-703-8	Sequence 8, Appl
156	6	2.2	273	1	US-08-137-175A-5	Sequence 5, Appl	229	6	2.2	348	4	US-09-415-277C-14	Sequence 14, Appl
157	6	2.2	273	3	US-08-479-017-5	Sequence 5, Appl	230	6	2.2	348	4	US-09-328-352-5513	Sequence 5513, Ap
158	6	2.2	273	3	US-09-196-293-13	Sequence 13, Appl	231	6	2.2	349	4	US-09-134-001C-4884	Sequence 4884, Ap
159	6	2.2	273	3	US-08-209-603E-13	Sequence 13, Appl	232	6	2.2	349	4	US-09-300-971A-9	Sequence 9, Appl
160	6	2.2	273	3	US-08-235-836C-11	Sequence 11, Appl	233	6	2.2	349	4	US-09-328-352-5364	Sequence 5364, Ap
161	6	2.2	273	3	US-08-235-836C-89	Sequence 89, Appl	234	6	2.2	354	1	US-08-753-233-2	Sequence 2, Appl
162	6	2.2	273	3	US-08-235-836C-140	Sequence 140, App	235	6	2.2	354	2	US-08-984-246-2	Sequence 2, Appl
163	6	2.2	273	3	US-08-235-836C-142	Sequence 142, App	236	6	2.2	354	2	US-09-149-674-2	Sequence 2, Appl
164	6	2.2	273	3	US-08-235-836C-144	Sequence 144, App	237	6	2.2	355	4	US-09-580-929-5	Sequence 5, Appl
165	6	2.2	273	6	5512669-11-546-13	Sequence 13, Appl	238	6	2.2	356	4	US-09-252-991A-19932	Sequence 19932, A
166	6	2.2	273	6	5512669-4	Patent No. 5512669	239	6	2.2	357	3	US-08-467-021-95	Sequence 95, Appl
167	6	2.2	275	4	US-09-252-991A-27808	Sequence 27808, A	240	6	2.2	357	3	US-09-025-580-24	Sequence 24, Appl
168	6	2.2	286	4	US-09-328-352-7001	Sequence 7001, Ap	241	6	2.2	357	4	US-09-025-580-24	Sequence 24, Appl
169	6	2.2	288	4	US-09-216-393B-341	Sequence 341, App	242	6	2.2	357	4	US-09-157-040B-13	Sequence 13, Appl
170	6	2.2	288	4	US-09-216-393B-341	Sequence 341, App	243	6	2.2	357	4	US-09-157-040B-13	Sequence 13, Appl
171	6	2.2	291	4	US-09-107-532A-7234	Sequence 7234, Ap	244	6	2.2	368	4	US-09-252-991A-26164	Sequence 26164, A
172	6	2.2	292	4	US-09-468-738A-2	Sequence 2, Appl	245	6	2.2	369	4	US-09-252-991A-31852	Sequence 31852, A
173	6	2.2	292	4	US-09-940-019-2	Sequence 2, Appl	246	6	2.2	369	4	US-09-107-532A-5270	Sequence 5270, Ap



247	6	2.2	370	3	US-08-467-023-97	Sequence 97, Appl	320	6	2.2	467	3	US-09-046-736-2	Sequence 2, Appl
248	6	2.2	372	1	US-08-753-233-3	Sequence 3, Appl	321	6	2.2	471	4	US-09-328-532-5408	Sequence 5408, Ap
249	6	2.2	372	2	US-08-984-246-3	Sequence 3, Appl	322	6	2.2	471	4	US-09-107-332A-4629	Sequence 4629, Ap
250	6	2.2	372	2	US-09-149-674-3	Sequence 3, Appl	323	6	2.2	472	4	US-09-252-991A-26992	Sequence 26992, A
251	6	2.2	372	4	US-09-252-991A-29108	Sequence 29108, A	324	6	2.2	474	3	US-08-729-416C-1	Sequence 1, Appl
252	6	2.2	373	4	US-09-574-141A-57	Sequence 57, Appl	325	6	2.2	474	3	US-08-729-416C-11	Sequence 11, Appl
253	6	2.2	374	3	US-08-467-033-2	Sequence 2, Appl	326	6	2.2	474	3	US-08-807-342B-2	Sequence 2, Appl
254	6	2.2	374	3	US-09-046-736-4	Sequence 4, Appl	327	6	2.2	474	4	US-09-433-353-1	Sequence 1, Appl
255	6	2.2	377	3	US-09-352-990-28	Sequence 28, Appl	328	6	2.2	474	4	US-09-433-353-11	Sequence 11, Appl
256	6	2.2	385	4	US-09-570-778A-12	Sequence 12, Appl	329	6	2.2	474	4	US-09-252-991A-29269	Sequence 29269, A
257	6	2.2	385	4	US-09-991-138-12	Sequence 12, Appl	330	6	2.2	476	3	US-09-233-989-2	Sequence 2, Appl
258	6	2.2	386	4	US-09-383-318A-2	Sequence 2, Appl	331	6	2.2	476	3	US-09-233-989-3	Sequence 3, Appl
259	6	2.2	387	1	US-07-637-870-3	Sequence 3, Appl	332	6	2.2	476	3	US-09-233-989-6	Sequence 6, Appl
260	6	2.2	387	1	US-07-637-399-9	Sequence 9, Appl	333	6	2.2	477	4	US-09-252-991A-27516	Sequence 27516, A
261	6	2.2	387	1	US-07-640-476-12	Sequence 12, Appl	334	6	2.2	479	4	US-09-252-991A-25982	Sequence 25982, A
262	6	2.2	387	1	US-08-112-703-9	Sequence 9, Appl	335	6	2.2	479	4	US-09-328-352-4361	Sequence 4361, Ap
263	6	2.2	388	4	US-09-107-532A-5369	Sequence 5369, Ap	336	6	2.2	483	3	US-09-108-020-16	Sequence 16, Appl
264	6	2.2	393	1	US-08-029-404-2	Sequence 2, Appl	337	6	2.2	483	4	US-09-252-991A-29267	Sequence 29267, A
265	6	2.2	393	3	US-08-459-953A-2	Sequence 2, Appl	338	6	2.2	485	2	US-08-477-451-22	Sequence 22, Appl
266	6	2.2	393	4	US-09-331-924-8	Sequence 8, Appl	339	6	2.2	489	4	US-09-328-352-5088	Sequence 5088, Ap
267	6	2.2	393	4	US-09-393-212-2	Sequence 2, Appl	340	6	2.2	489	4	US-09-252-991A-24949	Sequence 24949, A
268	6	2.2	394	2	US-08-555-568B-17	Sequence 17, Appl	341	6	2.2	495	3	US-09-079-415-4	Sequence 4, Appl
269	6	2.2	394	3	US-09-519-223-17	Sequence 17, Appl	342	6	2.2	497	4	US-09-252-991A-22660	Sequence 22660, A
270	6	2.2	402	1	US-08-553-703A-1	Sequence 1, Appl	343	6	2.2	499	2	US-07-952-853-6	Sequence 6, Appl
271	6	2.2	402	1	US-08-553-703A-4	Sequence 4, Appl	344	6	2.2	499	2	US-08-914-848-6	Sequence 6, Appl
272	6	2.2	402	2	US-09-006-021-1	Sequence 1, Appl	345	6	2.2	500	1	US-07-755-573C-8	Sequence 8, Appl
273	6	2.2	402	2	US-09-006-021-4	Sequence 4, Appl	346	6	2.2	500	4	US-09-519-878-2	Sequence 2, Appl
274	6	2.2	404	3	US-08-459-953A-7	Sequence 7, Appl	347	6	2.2	511	3	US-08-931-952-4	Sequence 4, Appl
275	6	2.2	404	4	US-08-393-212-7	Sequence 7, Appl	348	6	2.2	511	3	US-08-272-247-4	Sequence 4, Appl
276	6	2.2	406	4	US-09-252-991A-20630	Sequence 20630, A	349	6	2.2	511	5	PCT-US95-08560-4	Sequence 4, Appl
277	6	2.2	414	3	US-09-067-626-4	Sequence 4, Appl	350	6	2.2	515	4	US-09-252-991A-27942	Sequence 27942, A
278	6	2.2	414	4	US-09-252-991A-21108	Sequence 21108, A	351	6	2.2	515	4	US-09-107-532A-6214	Sequence 6214, Ap
279	6	2.2	414	4	US-09-107-532A-7057	Sequence 7057, Ap	352	6	2.2	516	1	US-08-356-340-4	Sequence 4, Appl
280	6	2.2	417	1	US-08-553-703A-2	Sequence 2, Appl	353	6	2.2	516	2	US-08-786-555-4	Sequence 4, Appl
281	6	2.2	417	2	US-09-006-021-2	Sequence 2, Appl	354	6	2.2	521	4	US-09-252-991A-27321	Sequence 27321, A
282	6	2.2	417	4	US-09-328-352-6981	Sequence 6981, Ap	355	6	2.2	526	4	US-09-252-991A-20533	Sequence 20533, A
283	6	2.2	419	1	US-08-553-703A-3	Sequence 3, Appl	356	6	2.2	533	3	US-09-350-268-3	Sequence 3, Appl
284	6	2.2	419	2	US-09-006-021-3	Sequence 3, Appl	357	6	2.2	533	4	US-09-558-679-3	Sequence 3, Appl
285	6	2.2	422	4	US-09-252-991A-32607	Sequence 32607, A	358	6	2.2	533	4	US-09-347-650-17	Sequence 17, Appl
286	6	2.2	423	2	US-08-715-554-2	Sequence 2, Appl	359	6	2.2	534	3	US-09-124-541-1	Sequence 1, Appl
287	6	2.2	423	2	US-08-583-118-2	Sequence 2, Appl	360	6	2.2	535	4	US-09-252-991A-24728	Sequence 24728, A
288	6	2.2	425	4	US-09-252-991A-19692	Sequence 19692, A	361	6	2.2	545	4	US-08-976-063B-10	Sequence 10, Appl
289	6	2.2	432	4	US-09-443-041A-20	Sequence 20, Appl	362	6	2.2	558	4	US-09-252-991A-26115	Sequence 26115, A
290	6	2.2	433	4	US-09-252-991A-30888	Sequence 30888, A	363	6	2.2	558	4	US-09-252-991A-28571	Sequence 28571, A
291	6	2.2	435	1	US-08-111-939-14	Sequence 14, Appl	364	6	2.2	569	4	US-09-252-991A-29263	Sequence 29263, A
292	6	2.2	435	1	US-08-111-939-15	Sequence 15, Appl	365	6	2.2	572	4	US-09-252-991A-17898	Sequence 17898, A
293	6	2.2	435	1	US-08-111-939-16	Sequence 16, Appl	366	6	2.2	582	3	US-09-272-414-2	Sequence 2, Appl
294	6	2.2	435	1	US-08-452-262-2	Sequence 2, Appl	367	6	2.2	585	2	US-08-453-848-11	Sequence 11, Appl
295	6	2.2	435	1	US-08-734-550-2	Sequence 2, Appl	368	6	2.2	585	3	US-09-169-027-11	Sequence 11, Appl
296	6	2.2	435	5	PCT-US96-07528-2	Sequence 2, Appl	369	6	2.2	586	2	US-08-453-848-19	Sequence 19, Appl
297	6	2.2	437	4	US-09-252-991A-18636	Sequence 18636, A	370	6	2.2	586	3	US-09-169-027-19	Sequence 19, Appl
298	6	2.2	438	3	US-08-486-099-93	Sequence 93, Appl	371	6	2.2	589	2	US-08-453-848-13	Sequence 13, Appl
299	6	2.2	438	3	US-08-360-107A-103	Sequence 103, App	372	6	2.2	589	3	US-09-169-027-13	Sequence 13, Appl
300	6	2.2	438	3	US-08-484-223B-93	Sequence 93, Appl	373	6	2.2	589	4	US-09-740-041-2	Sequence 2, Appl
301	6	2.2	438	3	US-08-919-597-93	Sequence 93, Appl	374	6	2.2	592	3	US-08-453-848-17	Sequence 17, Appl
302	6	2.2	438	3	US-08-475-668A-93	Sequence 93, Appl	375	6	2.2	592	3	US-09-169-027-17	Sequence 17, Appl
303	6	2.2	438	3	US-08-485-551A-93	Sequence 93, Appl	376	6	2.2	594	3	US-08-729-416C-7	Sequence 7, Appl
304	6	2.2	438	3	US-08-471-913A-93	Sequence 93, Appl	377	6	2.2	594	3	US-08-729-416C-17	Sequence 17, Appl
305	6	2.2	438	3	US-08-485-264A-93	Sequence 93, Appl	378	6	2.2	594	4	US-09-433-353-7	Sequence 7, Appl
306	6	2.2	438	4	US-08-474-349A-93	Sequence 93, Appl	379	6	2.2	594	4	US-09-433-353-17	Sequence 17, Appl
307	6	2.2	438	4	US-08-255-208A-29	Sequence 29, Appl	380	6	2.2	598	4	US-09-252-991A-28599	Sequence 28599, A
308	6	2.2	438	4	US-08-470-896-93	Sequence 93, Appl	381	6	2.2	607	3	US-09-335-409-9	Sequence 9, Appl
309	6	2.2	438	4	US-08-485-546A-93	Sequence 93, Appl	382	6	2.2	607	4	US-09-568-102-9	Sequence 9, Appl
310	6	2.2	439	4	US-09-252-991A-27662	Sequence 27662, A	383	6	2.2	607	4	US-09-567-969-9	Sequence 9, Appl
311	6	2.2	441	4	US-09-252-991A-20573	Sequence 20573, A	384	6	2.2	607	4	US-09-568-480-9	Sequence 9, Appl
312	6	2.2	441	4	US-09-328-352-5426	Sequence 5426, Ap	385	6	2.2	607	4	US-09-568-486-9	Sequence 9, Appl
313	6	2.2	441	4	US-09-328-352-6745	Sequence 6745, Ap	386	6	2.2	607	4	US-09-568-472-9	Sequence 9, Appl
314	6	2.2	443	4	US-09-252-991A-21563	Sequence 21563, A	387	6	2.2	607	4	US-09-567-899-9	Sequence 9, Appl
315	6	2.2	448	4	US-09-252-991A-31398	Sequence 31398, A	388	6	2.2	613	4	US-09-252-991A-21411	Sequence 21411, A
316	6	2.2	449	4	US-09-984-880-2	Sequence 2, Appl	389	6	2.2	619	3	US-09-156-253-48	Sequence 48, Appl
317	6	2.2	457	4	US-09-252-991A-20955	Sequence 20955, A	390	6	2.2	619	5	PCT-US93-03027-6	Sequence 6, Appl
318	6	2.2	462	3	US-09-238-796-2	Sequence 2, Appl	391	6	2.2	628	4	US-09-252-991A-22131	Sequence 22131, A
319	6	2.2	465	4	US-09-134-001C-4428	Sequence 4428, Ap	392	6	2.2	632	4	US-09-252-991A-23096	Sequence 23096, A

393	6	2.2	633	2	US-08-736-770-3	Sequence 3, Appli	466	6	2.2	1065	4	US-09-252-991A-31637	Sequence 31637, A
394	6	2.2	633	2	US-08-557-006C-43	Sequence 43, Appli	467	6	2.2	1072	3	US-09-357-251-31	Sequence 31, Appl
395	6	2.2	636	4	US-09-165-558-60	Sequence 60, Appl	468	6	2.2	1073	4	US-09-206-942-49	Sequence 49, Appl
396	6	2.2	648	4	US-09-153-637A-221	Sequence 221, App	469	6	2.2	1074	4	US-08-768-147B-2	Sequence 2, Appli
397	6	2.2	652	4	US-09-252-991A-30597	Sequence 30597, A	470	6	2.2	1074	3	US-08-968-752B-2	Sequence 2, Appli
398	6	2.2	654	4	US-09-134-001C-3261	Sequence 3261, Ap	471	6	2.2	1074	3	US-08-107-749-3	Sequence 2, Appli
399	6	2.2	655	4	US-09-252-991A-28411	Sequence 28411, A	472	6	2.2	1074	4	US-08-536-424-2	Sequence 2, Appli
400	6	2.2	656	4	US-09-327-984A-36	Sequence 36, Appl	473	6	2.2	1079	4	US-08-206-942-47	Sequence 47, Appl
401	6	2.2	656	4	US-09-134-001C-4322	Sequence 4322, Ap	474	6	2.2	1088	4	US-08-742-026-2	Sequence 2, Appl
402	6	2.2	659	4	US-09-562-737-12	Sequence 12, Appl	475	6	2.2	1088	2	US-08-742-026-23	Sequence 23, Appl
403	6	2.2	660	4	US-09-107-532A-6715	Sequence 6715, Ap	476	6	2.2	1125	4	US-09-328-352-8233	Sequence 8233, Ap
404	6	2.2	662	1	US-08-224-657-88	Sequence 88, Appl	477	6	2.2	1221	4	US-09-107-532A-3959	Sequence 3959, Ap
405	6	2.2	662	4	US-09-354-138-88	Sequence 88, Appl	478	6	2.2	1234	2	US-08-936-545-2	Sequence 2, Appli
406	6	2.2	686	2	US-08-993-228-12	Sequence 12, Appl	479	6	2.2	1334	3	US-09-328-320-2	Sequence 2, Appli
407	6	2.2	687	2	US-08-555-568B-21	Sequence 21, Appl	480	6	2.2	1334	3	US-09-722-139-2	Sequence 2, Appli
408	6	2.2	687	3	US-09-519-223-21	Sequence 23, Appl	481	6	2.2	1375	4	US-09-721-832-2	Sequence 2, Appli
409	6	2.2	688	2	US-08-555-568B-23	Sequence 23, Appl	482	6	2.2	1375	4	US-09-721-832-2	Sequence 2, Appli
410	6	2.2	688	3	US-09-519-223-21	Sequence 23, Appl	483	6	2.2	1432	3	US-08-781-891-71	Sequence 71, Appl
411	6	2.2	693	1	US-08-463-620-11	Sequence 11, Appl	484	6	2.2	1432	4	US-09-618-166-71	Sequence 71, Appl
412	6	2.2	693	2	US-08-224-917-11	Sequence 11, Appl	485	6	2.2	1581	3	US-09-110-517-2	Sequence 2, Appli
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414	6	2.2	693	5	PCT-US95-0393A-11	Sequence 11, Appl	487	6	2.2	1706	3	US-08-399-411-2	Sequence 2, Appli
415	6	2.2	716	4	US-09-252-991A-21498	Sequence 21498, A	488	6	2.2	1706	3	US-08-516-859A-2	Sequence 2, Appli
416	6	2.2	742	4	US-09-500-123-12	Sequence 12, Appl	489	6	2.2	1706	4	US-09-588-706-2	Sequence 2, Appli
417	6	2.2	742	4	US-08-252-991A-24489	Sequence 24489, A	490	6	2.2	1706	4	US-09-588-706-2	Sequence 2, Appli
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420	6	2.2	752	2	US-08-735-176-2	Sequence 2, Appli	493	6	2.2	1784	3	US-08-632-426A-2	Sequence 2, Appli
421	6	2.2	752	2	US-08-555-568B-2	Sequence 2, Appli	494	6	2.2	1788	2	US-08-962-284-2	Sequence 2, Appli
422	6	2.2	752	2	US-09-519-223-2	Sequence 2, Appli	495	6	2.2	1792	2	US-08-962-284-2	Sequence 2, Appli
423	6	2.2	752	5	PCT-US95-08069-2	Sequence 2, Appli	496	6	2.2	1810	4	US-08-793-273C-4	Sequence 4, Appli
424	6	2.2	765	3	US-08-444-818-70	Sequence 70, Appl	497	6	2.2	1810	5	PCT-US95-1168C-4	Sequence 4, Appli
425	6	2.2	768	2	US-08-560-398-2	Sequence 2, Appli	498	6	2.2	2071	3	US-09-415-522-6	Sequence 6, Appli
426	6	2.2	773	4	US-09-252-991A-19916	Sequence 2, Appli	499	6	2.2	2071	3	US-08-418-893D-23	Sequence 23, Appl
427	6	2.2	782	4	US-09-252-991A-21554	Sequence 21554, A	500	6	2.2	2089	1	US-08-418-893D-24	Sequence 24, Appl
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429	6	2.2	809	4	US-09-252-991A-29280	Sequence 29280, A	502	6	2.2	2647	2	US-08-779-113-8	Sequence 8, Appli
430	6	2.2	811	4	US-09-500-123-9	Sequence 9, Appli	503	6	2.2	2736	4	US-09-252-991A-30227	Sequence 30227, A
431	6	2.2	815	4	US-09-328-352-4284	Sequence 4284, Ap	504	6	2.2	2890	3	US-09-413-814-67	Sequence 67, Appl
432	6	2.2	817	1	US-07-640-029-2	Sequence 2, Appli	505	6	2.2	3077	6	523423-2	Patent No. 523423
433	6	2.2	821	4	US-09-252-991A-21013	Sequence 21013, A	506	6	2.2	3170	3	US-09-036-987A-4	Sequence 4, Appli
434	6	2.2	833	3	US-08-699-103B-4	Sequence 4, Appli	507	6	2.2	3170	3	US-09-370-700-4	Sequence 4, Appli
435	6	2.2	833	4	US-09-229-059-4	Sequence 4, Appli	508	6	2.2	3170	4	US-09-603-207-4	Sequence 4, Appli
436	6	2.2	833	4	US-09-628-133-4	Sequence 4, Appli	509	6	2.2	3572	2	US-08-822-445-12	Sequence 12, Appl
437	6	2.2	863	4	US-09-328-352-6730	Sequence 6730, Ap	510	6	2.2	3572	4	US-09-396-540-12	Sequence 12, Appl
438	6	2.2	869	4	US-09-252-991A-17678	Sequence 17678, A	511	6	2.2	3798	3	US-09-335-409-6	Sequence 6, Appli
439	6	2.2	871	4	US-09-500-123-7	Sequence 7, Appli	512	6	2.2	3798	4	US-09-588-102-6	Sequence 6, Appli
440	6	2.2	907	3	US-08-938-830-16	Sequence 26, Appl	513	6	2.2	3798	4	US-08-567-899-6	Sequence 6, Appli
441	6	2.2	907	3	US-09-020-222-26	Sequence 26, Appl	514	6	2.2	3798	4	US-08-568-486-6	Sequence 6, Appli
442	6	2.2	907	4	US-09-170-496D-264	Sequence 264, App	515	6	2.2	3798	4	US-09-588-486-6	Sequence 6, Appli
443	6	2.2	907	4	US-09-170-496D-278	Sequence 278, App	516	6	2.2	3798	4	US-08-567-899-6	Sequence 6, Appli
444	6	2.2	911	3	US-09-074-579-4	Sequence 4, Appli	517	6	2.2	3798	4	US-08-822-445-10	Sequence 10, Appl
445	6	2.2	911	3	US-09-389-774-4	Sequence 4, Appli	518	6	2.2	3801	2	US-09-396-540-10	Sequence 10, Appl
446	6	2.2	912	4	US-08-461-562B-2	Sequence 2, Appli	519	6	2.2	3801	4	US-09-180-422B-27	Sequence 27, Appl
447	6	2.2	912	4	US-09-252-991A-33129	Sequence 33129, A	520	6	2.2	4536	4	US-09-108-006C-1	Sequence 1, Appli
448	6	2.2	930	4	US-09-134-001C-5314	Sequence 5314, Ap	521	6	2.2	4563	4	US-09-108-006C-1	Sequence 1, Appli
449	6	2.2	944	4	US-09-449-285A-2	Sequence 2, Appli	522	6	2.2	4928	3	US-09-370-700-5	Sequence 5, Appli
450	6	2.2	951	4	US-09-252-991A-19440	Sequence 19440, A	523	6	2.2	4928	3	US-09-370-700-5	Sequence 5, Appli
451	6	2.2	954	4	US-09-351-150A-17	Sequence 17, Appl	524	6	2.2	4928	3	US-09-603-207-5	Sequence 5, Appli
452	6	2.2	971	3	US-09-107-149-19	Sequence 19, Appl	525	6	2.2	5087	3	US-09-144-085-1	Sequence 1, Appli
453	6	2.2	972	3	US-08-335-844A-23	Sequence 23, Appl	526	6	2.2	6095	3	US-09-144-085-2	Sequence 2, Appli
454	6	2.2	972	4	US-09-129-366-23	Sequence 23, Appl	527	5	1.8	7	4	US-09-374-454-16	Sequence 16, Appl
455	6	2.2	983	2	US-08-164-292B-26	Sequence 26, Appl	528	5	1.8	8	4	US-08-635-886C-143	Sequence 143, App
456	6	2.2	983	3	US-08-845-623-26	Sequence 26, Appl	529	5	1.8	9	2	US-08-986-234-69	Sequence 69, Appl
457	6	2.2	983	3	US-08-815-927-26	Sequence 26, Appl	530	5	1.8	9	4	US-09-492-543-61	Sequence 61, Appl
458	6	2.2	983	4	US-09-103-310-26	Sequence 26, Appl	531	5	1.8	9	4	US-09-492-543-118	Sequence 118, App
459	6	2.2	983	4	US-09-435-242-26	Sequence 26, Appl	532	5	1.8	9	4	US-09-492-543-117	Sequence 117, App
460	6	2.2	1027	4	US-09-252-991A-26494	Sequence 26494, A	533	5	1.8	9	4	US-09-355-304B-2	Sequence 2, Appli
461	6	2.2	1027	4	US-09-162-041B-21000	Sequence 21000, A	534	5	1.8	9	4	US-09-355-304B-2	Sequence 2, Appli
462	6	2.2	1033	4	US-09-252-991A-21000	Sequence 21000, A	535	5	1.8	9	4	US-09-359-304B-5	Sequence 5, Appli
463	6	2.2	1034	4	US-09-252-991A-28921	Sequence 28921, A	536	5	1.8	9	4	US-09-359-304B-5	Sequence 5, Appli
464	6	2.2	1036	3	US-08-968-752B-4	Sequence 4, Appli	537	5	1.8	9	4	US-09-510-751A-6	Sequence 6, Appli
465	6	2.2	1036	4	US-09-536-224-4	Sequence 4, Appli	538	5	1.8	9	4	US-09-510-751A-6	Sequence 6, Appli

539	5	1.8	9	4	US-09-344-040C-76	Sequence 76, Appl	612	5	1.8	20	4	US-09-161-939A-11	Sequence 11, Appl
540	5	1.8	10	2	US-08-276-967-8	Sequence 8, Appli	613	5	1.8	20	4	US-09-205-258-489	Sequence 489, App
541	5	1.8	10	3	US-08-996-338-16	Sequence 16, Appl	614	5	1.8	20	5	PCT-US95-02626-13	Sequence 13, Appl
542	5	1.8	10	4	US-09-556-972-16	Sequence 16, Appl	615	5	1.8	20	6	547657-6	Patent No. 547657
543	5	1.8	11	1	US-08-411-727-2	Sequence 2, Appli	616	5	1.8	21	2	US-08-480-190-235	Sequence 235, App
544	5	1.8	11	2	US-08-385-335A-5	Sequence 5, Appli	617	5	1.8	21	2	US-08-488-379-235	Sequence 235, App
545	5	1.8	11	3	US-09-206-059-22	Sequence 22, Appl	618	5	1.8	21	3	US-08-256-747C-37	Sequence 37, Appl
546	5	1.8	11	3	US-09-206-059-24	Sequence 24, Appl	619	5	1.8	21	3	US-08-834-130A-37	Sequence 37, Appl
547	5	1.8	12	1	US-08-443-642-7	Sequence 7, Appli	620	5	1.8	21	4	US-09-187-789-19	Sequence 19, Appl
548	5	1.8	12	2	US-08-637-759B-97	Sequence 97, Appl	621	5	1.8	21	4	US-08-924-629C-13	Sequence 13, Appl
549	5	1.8	12	3	US-08-871-355A-97	Sequence 97, Appl	622	5	1.8	21	4	US-09-139-600-14	Sequence 14, Appl
550	5	1.8	12	3	US-08-997-211-7	Sequence 7, Appli	623	5	1.8	21	4	US-09-555-313B-6	Sequence 6, Appli
551	5	1.8	12	4	US-09-201-945-97	Sequence 97, Appl	624	5	1.8	21	4	US-08-475-399A-235	Sequence 235, App
552	5	1.8	13	2	US-08-637-759B-193	Sequence 193, App	625	5	1.8	21	5	PCT-US93-07545-235	Sequence 235, App
553	5	1.8	13	3	US-08-871-355A-193	Sequence 193, App	626	5	1.8	22	1	US-08-460-874A-37	Sequence 37, Appl
554	5	1.8	13	3	US-08-928-383B-7	Sequence 7, Appli	627	5	1.8	22	2	US-08-388-883B-37	Sequence 37, Appl
555	5	1.8	13	4	US-09-201-945-193	Sequence 193, App	628	5	1.8	22	3	US-08-462-211A-37	Sequence 37, Appl
556	5	1.8	14	2	US-08-695-412B-2	Sequence 2, Appli	629	5	1.8	22	3	US-09-004-406C-32	Sequence 32, Appl
557	5	1.8	14	2	US-08-937-102-25	Sequence 25, Appl	630	5	1.8	23	2	US-08-480-190-157	Sequence 157, App
558	5	1.8	14	3	US/08/622	INFORMATION FOR	631	5	1.8	23	2	US-08-480-190-157	Sequence 157, App
559	5	1.8	14	3	US-08-960-190A-29	Sequence 29, Appl	632	5	1.8	23	2	US-08-488-379-157	Sequence 157, App
560	5	1.8	14	4	US-09-165-922A-2	Sequence 2, Appli	633	5	1.8	23	2	US-08-488-379-274	Sequence 274, App
561	5	1.8	15	1	US-07-907-190-4	Sequence 4, Appli	634	5	1.8	23	4	US-08-475-399A-157	Sequence 157, App
562	5	1.8	15	1	US-08-442-063A-1	Sequence 1, Appli	635	5	1.8	23	4	US-08-475-399A-274	Sequence 274, App
563	5	1.8	15	1	US-08-442-063A-21	Sequence 21, Appl	636	5	1.8	23	4	US-09-281-495-1	Sequence 1, Appli
564	5	1.8	15	2	US-08-695-412B-1	Sequence 1, Appli	637	5	1.8	23	5	PCT-US93-07545-18	Sequence 18, Appl
565	5	1.8	15	2	US-08-683-262B-70	Sequence 70, Appl	638	5	1.8	23	5	US-09-509-593-18	Sequence 18, Appl
566	5	1.8	15	2	US-08-937-102-23	Sequence 23, Appl	639	5	1.8	24	1	US-08-141-324-21	Sequence 21, Appl
567	5	1.8	15	2	US-08-937-102-24	Sequence 24, Appl	640	5	1.8	24	1	US-08-541-902-21	Sequence 21, Appl
568	5	1.8	15	3	US/08/622	GENERAL INFORMA	641	5	1.8	24	2	US-08-256-156A-2	Sequence 2, Appli
569	5	1.8	15	3	US-08-874-197-5	Sequence 5, Appli	642	5	1.8	24	2	US-08-679-405-5	Sequence 5, Appli
570	5	1.8	15	3	US-08-874-197-9	Sequence 9, Appli	643	5	1.8	24	2	US-08-842-799-5	Sequence 5, Appli
571	5	1.8	15	3	US-09-361-707-70	Sequence 70, Appl	644	5	1.8	24	3	US-08-855-958-6	Sequence 6, Appli
572	5	1.8	15	4	US-08-648-182-5	Sequence 5, Appli	645	5	1.8	24	5	PCT-US96-11459-5	Sequence 5, Appli
573	5	1.8	15	4	US-08-648-182-9	Sequence 9, Appli	646	5	1.8	25	1	US-08-614-935-69	Sequence 69, Appl
574	5	1.8	15	4	US-09-165-922A-1	Sequence 1, Appli	647	5	1.8	25	3	US-08-902-516-4	Sequence 4, Appli
575	5	1.8	15	4	US-09-490-702B-20	Sequence 20, Appl	648	5	1.8	25	3	US-09-130-287-69	Sequence 69, Appl
576	5	1.8	16	1	US-08-164-839-55	Sequence 55, Appl	649	5	1.8	25	4	US-09-847-185-4	Sequence 4, Appli
577	5	1.8	16	1	US-08-218-025A-12	Sequence 12, Appl	650	5	1.8	26	4	US-09-509-593-17	Sequence 17, Appl
578	5	1.8	16	1	US-08-583-799-55	Sequence 55, Appl	651	5	1.8	27	3	US-09-120-365-33	Sequence 33, Appl
579	5	1.8	16	2	US-08-385-335A-6	Sequence 6, Appli	652	5	1.8	27	3	US-09-515-039-33	Sequence 33, Appl
580	5	1.8	16	3	US-09-434-774-13	Sequence 13, Appl	653	5	1.8	27	4	US-09-509-593-16	Sequence 16, Appl
581	5	1.8	16	4	US-09-574-749B-58	Sequence 58, Appl	654	5	1.8	28	1	US-08-276-213-4	Sequence 4, Appli
582	5	1.8	17	2	US-08-480-190-236	Sequence 236, App	655	5	1.8	28	1	US-07-977-630-46	Sequence 46, Appl
583	5	1.8	17	2	US-08-637-763B-2	Sequence 2, Appli	656	5	1.8	28	1	US-08-440-391-2	Sequence 2, Appli
584	5	1.8	17	2	US-08-488-379-236	Sequence 236, App	657	5	1.8	28	1	US-08-440-391-18	Sequence 18, Appl
585	5	1.8	17	3	US-09-170-354-2	Sequence 2, Appli	658	5	1.8	28	2	US-08-908-597A-2	Sequence 2, Appli
586	5	1.8	17	4	US-08-475-399A-236	Sequence 236, App	659	5	1.8	28	2	US-08-908-597A-18	Sequence 18, Appl
587	5	1.8	17	5	PCT-US93-07545-236	Sequence 236, App	660	5	1.8	28	3	US-09-236-385A-2	Sequence 2, Appli
588	5	1.8	18	1	US-08-391-000-1	Sequence 1, Appli	661	5	1.8	28	3	PCT-US96-06122-2	Sequence 2, Appli
589	5	1.8	18	2	US-08-741-931-1	Sequence 1, Appli	662	5	1.8	28	5	US-09-236-385A-18	Sequence 18, Appl
590	5	1.8	18	2	US-08-923-274-17	Sequence 17, Appl	663	5	1.8	28	5	PCT-US96-06122-2	Sequence 2, Appli
591	5	1.8	18	2	US-08-959-536-17	Sequence 17, Appl	664	5	1.8	29	2	US-08-846-762-56	Sequence 56, Appl
592	5	1.8	18	4	US-09-447-125B-27	Sequence 27, Appl	665	5	1.8	29	2	US-08-846-762-65	Sequence 65, Appl
593	5	1.8	18	4	US-09-552-802B-27	Sequence 27, Appl	666	5	1.8	30	3	US-08-467-023-260	Sequence 260, App
594	5	1.8	19	4	US-08-990-888-15	Sequence 15, Appl	667	5	1.8	30	3	US-09-425-638A-101	Sequence 101, App
595	5	1.8	20	1	US-07-777-715-4	Sequence 4, Appli	668	5	1.8	30	4	BARTHOLD-	Sequence 4, Appli
596	5	1.8	20	1	US-08-205-338A-13	Sequence 13, Appl	669	5	1.8	30	4	US-09-543-004-101	Sequence 101, App
597	5	1.8	20	1	US-07-908-253-5	Sequence 5, Appli	670	5	1.8	30	4	US-09-205-258-521	Sequence 521, App
598	5	1.8	20	1	US-08-218-025A-59	Sequence 49, Appl	671	5	1.8	31	3	US-09-045-632-73	Sequence 73, Appl
599	5	1.8	20	1	US-08-218-025A-40	Sequence 50, Appl	672	5	1.8	31	3	US-08-190-802A-180	Sequence 180, App
600	5	1.8	20	1	US-08-170-126-6	Sequence 6, Appli	673	5	1.8	32	1	US-08-190-802A-181	Sequence 181, App
601	5	1.8	20	1	US-08-321-071A-19	Sequence 19, Appl	674	5	1.8	32	3	US-08-477-346-180	Sequence 180, App
602	5	1.8	20	1	US-08-306-116A-11	Sequence 11, Appl	675	5	1.8	32	3	US-08-477-346-181	Sequence 181, App
603	5	1.8	20	2	US-08-535-837-5	Sequence 5, Appli	676	5	1.8	32	4	US-08-473-089-180	Sequence 180, App
604	5	1.8	20	3	US-08-467-023-29	Sequence 29, Appl	677	5	1.8	32	4	US-08-473-089-181	Sequence 181, App
605	5	1.8	20	3	US-08-954-418-6	Sequence 6, Appli	678	5	1.8	32	4	US-08-487-072A-180	Sequence 180, App
606	5	1.8	20	3	US-08-602-999A-114	Sequence 114, App	679	5	1.8	32	4	US-08-487-072A-181	Sequence 181, App
607	5	1.8	20	4	US-09-439-313-494	Sequence 494, App	680	5	1.8	33	2	US-09-031-485-84	Sequence 84, Appl
608	5	1.8	20	4	US-09-304-799-2	Sequence 2, Appli	681	5	1.8	33	2	US-08-847-429A-84	Sequence 84, Appl
609	5	1.8	20	4	US-09-257-179-92	Sequence 92, Appl	682	5	1.8	33	2	US-08-640-847C-5	Sequence 5, Appli
610	5	1.8	20	4	US-09-500-124-114	Sequence 114, App	683	5	1.8	33	3	US-08-651-136C-30	Sequence 30, Appl
611	5	1.8	20	4	US-09-161-939A-10	Sequence 10, Appl	684	5	1.8	33	3	US-09-065-474-84	Sequence 84, Appl

685	1.8	33	4	US-09-557-034-84	Sequence 84, Appl	758	1.8	48	3	US-08-804-439A-105	Sequence 105, Appl
686	1.8	33	4	US-08-978-385-1	Sequence 1, Appl	759	1.8	48	3	US-09-004-406C-23	Sequence 23, Appl
687	1.8	33	4	US-09-229-911A-30	Sequence 30, Appl	760	1.8	48	3	US-09-042-071-26	Sequence 26, Appl
688	1.8	33	4	US-08-595-468-3	Sequence 3, Appl	761	1.8	48	4	US-09-461-325-143	Sequence 143, Appl
689	1.8	36	1	US-08-908-391-14	Sequence 14, Appl	762	1.8	48	4	US-09-205-258-1023	Sequence 1023, Appl
690	1.8	36	2	US-08-908-597A-14	Sequence 14, Appl	763	1.8	49	1	US-08-118-270-201	Sequence 201, Appl
691	1.8	36	3	US-08-365-385A-14	Sequence 14, Appl	764	1.8	49	1	US-08-262-037-65	Sequence 65, Appl
692	1.8	36	4	US-09-315-304B-1482	Sequence 1482, Appl	765	1.8	49	1	US-09-237-357-595	Sequence 595, Appl
693	1.8	36	4	US-08-288-143-130	Sequence 130, Appl	766	1.8	49	4	US-09-377-466B-27	Sequence 27, Appl
694	1.8	36	5	PCT-US96-06122-14	Sequence 14, Appl	767	1.8	49	4	PCT-US91-08528-201	Sequence 201, Appl
695	1.8	37	1	US-08-130-802A-169	Sequence 169, Appl	768	1.8	50	4	US-08-931-851-9	Sequence 9, Appl
696	1.8	37	1	US-08-130-802A-214	Sequence 214, Appl	769	1.8	51	2	US-08-322-825-29	Sequence 29, Appl
697	1.8	37	3	US-08-477-346-169	Sequence 169, Appl	770	1.8	51	2	US-08-466-361A-29	Sequence 29, Appl
698	1.8	37	3	US-08-477-346-214	Sequence 214, Appl	771	1.8	53	3	US-09-155-107-15	Sequence 15, Appl
699	1.8	37	4	US-08-473-089-169	Sequence 169, Appl	772	1.8	53	3	US-09-155-107-16	Sequence 16, Appl
700	1.8	37	4	US-08-473-089-214	Sequence 214, Appl	773	1.8	53	3	US-09-155-107-17	Sequence 17, Appl
701	1.8	37	4	US-08-487-072A-169	Sequence 169, Appl	774	1.8	53	3	US-09-155-107-18	Sequence 18, Appl
702	1.8	37	4	US-08-487-072A-214	Sequence 214, Appl	775	1.8	53	3	US-09-042-071-37	Sequence 37, Appl
703	1.8	38	1	US-08-176-500-70	Sequence 70, Appl	776	1.8	56	2	US-08-867-087B-29	Sequence 29, Appl
704	1.8	38	1	US-07-956-700B-41	Sequence 41, Appl	777	1.8	58	1	US-08-262-037-77	Sequence 77, Appl
705	1.8	38	1	US-07-956-700B-52	Sequence 52, Appl	778	1.8	58	1	US-08-274-366-2	Sequence 2, Appl
706	1.8	38	1	US-08-471-052A-70	Sequence 70, Appl	779	1.8	58	2	US-08-572-951-37	Sequence 37, Appl
707	1.8	38	1	US-08-262-037-55	Sequence 55, Appl	780	1.8	58	2	US-08-152-721B-19	Sequence 19, Appl
708	1.8	38	1	US-08-189-331-70	Sequence 70, Appl	781	1.8	58	3	US-08-735-491-5	Sequence 5, Appl
709	1.8	38	1	US-08-476-537-41	Sequence 41, Appl	782	1.8	58	3	US-08-941-445A-34	Sequence 34, Appl
710	1.8	38	1	US-08-476-537-52	Sequence 52, Appl	783	1.8	58	5	PCT-US95-07828-2	Sequence 2, Appl
711	1.8	38	1	US-08-485-607-41	Sequence 41, Appl	784	1.8	59	1	US-08-262-037-66	Sequence 66, Appl
712	1.8	38	1	US-08-485-607-52	Sequence 52, Appl	785	1.8	59	2	US-08-392-816-18	Sequence 18, Appl
713	1.8	38	2	US-08-471-939-70	Sequence 70, Appl	786	1.8	59	4	US-08-924-629C-74	Sequence 74, Appl
714	1.8	38	2	US-08-471-800-70	Sequence 70, Appl	787	1.8	60	4	US-09-702-705-799	Sequence 799, Appl
715	1.8	38	2	US-08-471-868-70	Sequence 70, Appl	788	1.8	60	4	US-09-736-457-799	Sequence 799, Appl
716	1.8	38	2	US-08-475-879-41	Sequence 41, Appl	789	1.8	60	4	US-09-736-457-799	Sequence 799, Appl
717	1.8	38	2	US-08-475-879-52	Sequence 52, Appl	790	1.8	61	4	US-09-736-457-799	Sequence 799, Appl
718	1.8	38	3	US-08-927-219-35	Sequence 35, Appl	791	1.8	61	4	US-09-736-457-799	Sequence 799, Appl
719	1.8	38	3	US-09-172-841-23	Sequence 23, Appl	792	1.8	63	2	US-08-338-530A-6	Sequence 6, Appl
720	1.8	38	4	US-09-433-043B-41	Sequence 41, Appl	793	1.8	63	3	US-09-061-026-16	Sequence 16, Appl
721	1.8	38	4	US-09-433-043B-52	Sequence 52, Appl	794	1.8	63	3	US-09-061-026-22	Sequence 22, Appl
722	1.8	38	4	US-08-951-621-23	Sequence 23, Appl	795	1.8	63	3	US-09-466-138-16	Sequence 16, Appl
723	1.8	39	1	US-08-262-037-64	Sequence 64, Appl	796	1.8	63	3	US-09-466-138-22	Sequence 22, Appl
724	1.8	39	1	US-09-220-528-49	Sequence 49, Appl	797	1.8	63	3	US-09-267-384-6	Sequence 6, Appl
725	1.8	40	2	US-08-807-332B-32	Sequence 32, Appl	798	1.8	63	4	US-09-134-001C-2886	Sequence 2886, Appl
726	1.8	40	3	US-09-154-083-16	Sequence 16, Appl	799	1.8	63	4	US-09-706-770-6	Sequence 6, Appl
727	1.8	40	3	US-09-338-876-32	Sequence 32, Appl	800	1.8	64	4	US-09-134-001C-5429	Sequence 5429, Appl
728	1.8	41	3	US-09-177-249-57	Sequence 57, Appl	801	1.8	64	4	US-09-252-991A-17573	Sequence 17573, Appl
729	1.8	41	4	US-09-399-913-40	Sequence 40, Appl	802	1.8	64	4	US-09-252-991A-25618	Sequence 25618, Appl
730	1.8	41	4	US-09-298-731-40	Sequence 40, Appl	803	1.8	64	4	US-09-328-352-4697	Sequence 4697, Appl
731	1.8	42	1	US-08-377-687-39	Sequence 39, Appl	804	1.8	64	4	US-09-107-532A-4834	Sequence 4834, Appl
732	1.8	42	2	US-08-377-687-39	Sequence 39, Appl	805	1.8	65	3	US-08-981-392-36	Sequence 36, Appl
733	1.8	42	3	US-08-971-982-39	Sequence 39, Appl	806	1.8	65	4	US-09-107-532A-6375	Sequence 6375, Appl
734	1.8	43	3	US-09-188-930-175	Sequence 175, Appl	807	1.8	66	4	US-09-205-258-520	Sequence 520, Appl
735	1.8	43	3	US-08-675-499A-10	Sequence 10, Appl	808	1.8	66	6	5252466-4	Patent No. 5252466
736	1.8	43	4	US-08-312-283C-175	Sequence 175, Appl	809	1.8	67	1	US-08-203-806B-12	Sequence 12, Appl
737	1.8	43	4	US-09-071-710-37	Sequence 37, Appl	810	1.8	67	3	US-08-243-575-4	Sequence 4, Appl
738	1.8	43	4	US-09-071-710-37	Sequence 37, Appl	811	1.8	67	4	US-09-017-754A-12	Sequence 12, Appl
739	1.8	44	3	US-09-525-397-37	Sequence 37, Appl	812	1.8	67	4	US-09-134-001C-5270	Sequence 5270, Appl
740	1.8	44	3	US-09-525-397-37	Sequence 37, Appl	813	1.8	67	4	US-09-482-273-144	Sequence 144, Appl
741	1.8	45	3	US-09-018-635-37	Sequence 37, Appl	814	1.8	67	4	US-09-328-352-5686	Sequence 5686, Appl
742	1.8	45	3	US-09-018-635-39	Sequence 39, Appl	815	1.8	67	4	US-09-107-532A-6754	Sequence 6754, Appl
743	1.8	45	4	US-09-912-962-37	Sequence 37, Appl	816	1.8	68	1	US-08-262-037-67	Sequence 67, Appl
744	1.8	45	4	US-09-912-962-39	Sequence 39, Appl	817	1.8	68	1	US-08-466-033-148	Sequence 148, Appl
745	1.8	46	1	US-08-463-128-41	Sequence 41, Appl	818	1.8	68	2	US-08-444-733-148	Sequence 148, Appl
746	1.8	46	3	US-08-463-128-41	Sequence 41, Appl	819	1.8	68	2	US-08-461-361-148	Sequence 148, Appl
747	1.8	46	3	US-08-857-076-83	Sequence 83, Appl	820	1.8	68	2	US-08-485-910-148	Sequence 148, Appl
748	1.8	47	1	US-08-118-270-203	Sequence 203, Appl	821	1.8	68	2	US-09-134-001C-3029	Sequence 3029, Appl
749	1.8	47	1	US-08-443-063A-30	Sequence 30, Appl	822	1.8	68	4	US-09-180-167A-13	Sequence 13, Appl
750	1.8	47	1	US-08-443-063A-51	Sequence 51, Appl	823	1.8	69	4	US-09-134-001C-3193	Sequence 3193, Appl
751	1.8	47	1	US-08-443-063A-54	Sequence 54, Appl	824	1.8	69	4	US-09-134-001C-3406	Sequence 3406, Appl
752	1.8	47	4	US-08-469-260A-600	Sequence 600, Appl	825	1.8	69	4	US-09-732-210-1122	Sequence 210, Appl
753	1.8	47	4	US-08-469-260A-600	Sequence 600, Appl	826	1.8	69	4	US-08-311-731A-215	Sequence 215, Appl
754	1.8	47	4	US-08-488-446-600	Sequence 600, Appl	827	1.8	69	4	US-08-858-207A-514	Sequence 514, Appl
755	1.8	47	4	US-08-488-446-600	Sequence 600, Appl	828	1.8	70	4	US-08-262-037-56	Sequence 56, Appl
756	1.8	47	5	PCT-US93-08528-203	Sequence 203, Appl	829	1.8	71	1	US-08-369-247-79	Sequence 79, Appl
757	1.8	48	1	US-07-835-860-1	Sequence 1, Appl	830	1.8	71	4		

831	5	1.8	72	3	US-09-383-586-38	Sequence 38, Appl	904	1.8	96	2	US-08-470-868A-35	Sequence 35, Appl
832	5	1.8	72	4	US-09-134-001C-3540	Sequence 3540, Ap	905	1.8	96	3	US-09-210-681-35	Sequence 35, Appl
833	5	1.8	75	4	US-09-450-072-70	Sequence 70, Appl	906	1.8	96	3	US-08-946-719A-35	Sequence 35, Appl
834	5	1.8	75	4	US-09-351-348-70	Sequence 70, Appl	907	1.8	96	4	US-03-547-983-35	Sequence 35, Appl
835	5	1.8	76	1	US-08-848-252-4	Sequence 39, Appl	908	1.8	97	1	US-08-262-037-61	Sequence 61, Appl
836	5	1.8	76	4	US-09-020-846-39	Sequence 39, Appl	909	1.8	97	4	US-09-107-532A-6903	Sequence 6903, Ap
837	5	1.8	76	4	US-09-328-352-6085	Sequence 6085, Ap	910	1.8	97	4	US-09-107-532A-7243	Sequence 7243, Ap
838	5	1.8	77	1	US-08-262-037-68	Sequence 68, Appl	911	1.8	98	4	US-08-454-557C-30	Sequence 30, Appl
839	5	1.8	77	2	US-08-726-306A-32	Sequence 32, Appl	912	1.8	98	2	US-08-340-626C-30	Sequence 30, Appl
840	5	1.8	77	4	US-09-328-352-4275	Sequence 4275, Ap	913	1.8	98	2	US-08-450-673C-30	Sequence 30, Appl
841	5	1.8	77	4	US-09-328-352-5944	Sequence 5944, Ap	914	1.8	98	2	US-08-481-658B-50	Sequence 50, Appl
842	5	1.8	78	1	US-07-991-867B-4	Sequence 4, Appl	915	1.8	98	2	US-08-477-504A-50	Sequence 50, Appl
843	5	1.8	78	1	US-08-107-755A-4	Sequence 4, Appl	916	1.8	98	2	US-08-486-756A-50	Sequence 50, Appl
844	5	1.8	78	2	US-08-544-332-4	Sequence 4, Appl	917	1.8	98	2	US-08-485-862B-50	Sequence 50, Appl
845	5	1.8	78	4	US-09-370-861A-4	Sequence 4, Appl	918	1.8	98	3	US-08-487-077A-50	Sequence 50, Appl
846	5	1.8	78	4	US-09-107-532A-5823	Sequence 5823, Ap	919	1.8	98	3	US-08-485-863A-50	Sequence 50, Appl
847	5	1.8	78	4	US-09-107-532A-7263	Sequence 7263, Ap	920	1.8	98	3	US-08-485-049D-50	Sequence 50, Appl
848	5	1.8	79	1	US-08-665-220-68	Sequence 68, Appl	921	1.8	98	4	US-09-147-857-3	Sequence 3, Appl
849	5	1.8	79	2	US-09-174-060-5	Sequence 5, Appl	922	1.8	98	4	US-09-134-001C-4312	Sequence 4312, Ap
850	5	1.8	79	3	US-09-053-197A-15	Sequence 15, Appl	923	1.8	98	4	US-09-252-991A-23171	Sequence 23171, A
851	5	1.8	79	3	US-08-338-382-5	Sequence 5, Appl	924	1.8	98	5	PCT-US95-17111A-30	Sequence 30, Appl
852	5	1.8	79	3	US-09-291-692-68	Sequence 68, Appl	925	1.8	99	2	US-08-858-767-28	Sequence 28, Appl
853	5	1.8	79	4	US-09-085-761A-15	Sequence 15, Appl	926	1.8	99	2	US-08-863-028-28	Sequence 28, Appl
854	5	1.8	79	4	US-09-186-002-4	Sequence 4, Appl	927	1.8	99	4	US-09-370-838-95	Sequence 95, Appl
855	5	1.8	79	4	US-09-377-466B-26	Sequence 26, Appl	928	1.8	99	4	US-09-634-238-305	Sequence 305, App
856	5	1.8	79	4	US-09-252-991A-21406	Sequence 21406, A	929	1.8	99	4	US-09-252-991A-18340	Sequence 18340, A
857	5	1.8	79	4	US-09-107-532A-5614	Sequence 5614, Ap	930	1.8	100	4	US-09-397-787-18	Sequence 18, Appl
858	5	1.8	80	1	US-08-848-252-2	Sequence 2, Appl	931	1.8	100	4	US-09-198-452A-1076	Sequence 1076, Ap
859	5	1.8	81	4	US-09-252-991A-18646	Sequence 18646, A	932	1.8	100	4	US-09-886-319A-16	Sequence 16, Appl
860	5	1.8	81	4	US-09-198-452A-1027	Sequence 1027, Ap	933	1.8	101	1	US-08-220-401-5	Sequence 5, Appl
861	5	1.8	82	3	US-09-014-438-1	Sequence 1, Appl	934	1.8	101	3	US-08-437-362-5	Sequence 5, Appl
862	5	1.8	82	4	US-09-482-273-156	Sequence 156, App	935	1.8	101	3	US-09-374-135-6	Sequence 6, Appl
863	5	1.8	83	3	US-09-382-155-12	Sequence 12, Appl	936	1.8	101	4	US-09-599-160B-119	Sequence 119, App
864	5	1.8	83	3	US-09-074-044A-12	Sequence 12, Appl	937	1.8	101	4	US-09-107-532A-3974	Sequence 3974, Ap
865	5	1.8	83	4	US-08-198-452A-21	Sequence 21, Appl	938	1.8	102	4	US-09-732-210-1283	Sequence 1283, Ap
866	5	1.8	83	4	US-09-328-352-5531	Sequence 5531, Ap	939	1.8	103	4	US-08-924-629C-39	Sequence 39, Appl
867	5	1.8	83	4	US-09-107-532A-4957	Sequence 4957, Ap	940	1.8	103	4	US-09-107-532A-4967	Sequence 4967, Ap
868	5	1.8	84	3	US-09-107-532A-7177	Sequence 7177, Ap	941	1.8	105	1	US-08-241-853-11	Sequence 11, Appl
869	5	1.8	84	3	US-09-107-858-27	Sequence 27, Appl	942	1.8	105	2	US-08-850-917-11	Sequence 11, Appl
870	5	1.8	84	3	US-09-386-493-14	Sequence 14, Appl	943	1.8	105	4	US-09-025-769B-166	Sequence 166, App
871	5	1.8	84	4	US-08-439-313-571	Sequence 571, App	944	1.8	105	4	US-09-252-991A-27412	Sequence 27412, A
872	5	1.8	84	4	US-09-252-991A-19809	Sequence 19809, A	945	1.8	105	4	US-09-328-352-4390	Sequence 4390, Ap
873	5	1.8	84	4	US-09-328-352-5661	Sequence 5661, Ap	946	1.8	105	2	US-08-378-939-40	Sequence 40, Appl
874	5	1.8	85	4	US-09-134-001C-5110	Sequence 5110, Ap	947	1.8	106	2	US-08-378-939-42	Sequence 42, Appl
875	5	1.8	85	4	US-08-311-731A-323	Sequence 323, App	948	1.8	106	2	US-08-761-277A-49	Sequence 49, Appl
876	5	1.8	85	4	US-09-107-532A-3695	Sequence 3695, Ap	949	1.8	106	3	US-08-444-644-26	Sequence 26, Appl
877	5	1.8	86	3	US-08-905-223-429	Sequence 429, App	950	1.8	106	3	US-08-946-329A-76	Sequence 76, Appl
878	5	1.8	89	1	US-08-181-556-2	Sequence 2, Appl	951	1.8	106	4	US-08-232-246A-26	Sequence 26, Appl
879	5	1.8	89	4	US-08-686-878A-21	Sequence 21, Appl	952	1.8	106	4	US-08-936-165A-482	Sequence 482, App
880	5	1.8	89	4	US-09-175-928-21	Sequence 21, Appl	953	1.8	106	4	US-09-107-532A-5357	Sequence 5357, Ap
881	5	1.8	89	4	US-09-453-956-4	Sequence 4, Appl	954	1.8	107	1	US-07-893-929A-6	Sequence 6, Appl
882	5	1.8	89	4	US-09-252-991A-22408	Sequence 22408, A	955	1.8	107	1	US-08-422-101-8	Sequence 8, Appl
883	5	1.8	90	1	US-08-591-498-13	Sequence 13, Appl	956	1.8	107	1	US-08-422-091-8	Sequence 8, Appl
884	5	1.8	90	4	US-09-328-352-6160	Sequence 6160, Ap	957	1.8	107	2	US-08-422-092-8	Sequence 8, Appl
885	5	1.8	90	6	5218099-3	Patent No. 5218099	958	1.8	107	2	US-08-788-800-5	Sequence 5, Appl
886	5	1.8	91	4	US-09-424-311-4	Sequence 4, Appl	959	1.8	107	2	US-08-422-093-8	Sequence 8, Appl
887	5	1.8	91	4	US-08-983-502-22	Sequence 22, Appl	960	1.8	107	3	US-08-422-112-8	Sequence 8, Appl
888	5	1.8	91	4	US-08-983-502-34	Sequence 34, Appl	961	1.8	107	3	US-09-102-528-23	Sequence 23, Appl
889	5	1.8	91	4	US-09-516-747-22	Sequence 22, Appl	962	1.8	107	3	US-09-102-528-27	Sequence 27, Appl
890	5	1.8	91	5	US-09-516-747-34	Sequence 34, Appl	963	1.8	107	4	US-09-134-001C-2849	Sequence 2849, Ap
891	5	1.8	91	5	PCT-US96-10521-22	Sequence 22, Appl	964	1.8	107	4	US-09-301-593-20	Sequence 20, Appl
892	5	1.8	91	5	PCT-US96-10521-34	Sequence 34, Appl	965	1.8	107	5	US-09-461-325-484	Sequence 484, App
893	5	1.8	92	1	US-08-319-387-3	Sequence 3, Appl	966	1.8	107	5	PCT-US92-10344-6	Sequence 6, Appl
894	5	1.8	92	4	US-08-936-165A-313	Sequence 313, App	967	1.8	108	4	US-09-313-942-13	Sequence 13, Appl
895	5	1.8	92	4	US-09-370-838-211	Sequence 211, App	968	1.8	109	1	US-08-436-463-8	Sequence 8, Appl
896	5	1.8	93	4	US-09-312-283C-421	Sequence 421, App	969	1.8	109	1	US-08-024-253-8	Sequence 8, Appl
897	5	1.8	93	4	US-09-107-532A-5880	Sequence 5880, Ap	970	1.8	109	2	US-08-646-981-6	Sequence 6, Appl
898	5	1.8	94	1	US-08-262-037-57	Sequence 57, Appl	971	1.8	109	3	US-08-982-493-2	Sequence 2, Appl
899	5	1.8	94	3	US-08-232-878-4	Sequence 4, Appl	972	1.8	109	3	US-09-188-930-329	Sequence 329, App
900	5	1.8	96	1	US-08-538-878B-35	Sequence 35, Appl	973	1.8	109	4	US-09-199-637A-89	Sequence 89, Appl
901	5	1.8	96	1	US-08-442-063A-33	Sequence 33, Appl	974	1.8	109	4	US-09-399-913-34	Sequence 34, Appl
902	5	1.8	96	1	US-08-294-522B-34	Sequence 34, Appl	975	1.8	109	4	US-09-298-731-34	Sequence 34, Appl
903	5	1.8	96	2	US-08-807-861A-35	Sequence 35, Appl	976	1.8	109	4	US-09-312-283C-329	Sequence 329, App

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977 1.8 109 4 US-09-312-283C-422 Sequence 422, App
978 1.8 110 4 US-08-311-731A-334 Sequence 334, App
979 1.8 111 1 US-08-466-886-40 Sequence 40, Appl
980 1.8 111 3 US-08-545-809A-121 Sequence 121, App
981 1.8 111 3 US-08-469-617-40 Sequence 40, Appl
982 1.8 111 3 US-09-220-528-53 Sequence 53, Appl
983 1.8 111 4 US-09-198-452A-1158 Sequence 1158, App
984 1.8 111 4 US-09-732-210-244 Sequence 244, App
985 1.8 112 2 US-08-577-492-37 Sequence 37, Appl
986 1.8 112 2 US-08-933-750C-43 Sequence 43, Appl
987 1.8 112 3 US-09-234-613-43 Sequence 43, Appl
988 1.8 112 3 US-09-079-630-37 Sequence 37, Appl
989 1.8 112 4 US-09-395-689-6 Sequence 6, Appl
990 1.8 112 4 US-09-462-843A-4 Sequence 4, Appl
991 1.8 112 4 US-09-328-352-8222 Sequence 8222, App
992 1.8 112 4 US-08-311-731A-244 Sequence 244, App
993 1.8 113 4 US-09-311-352B-2 Sequence 2, Appl
994 1.8 114 4 US-09-574-141A-81 Sequence 81, Appl
995 1.8 116 2 US-08-879-995A-4 Sequence 4, Appl
996 1.8 116 3 US-09-215-096-4 Sequence 4, Appl
997 1.8 116 4 US-08-936-165A-304 Sequence 304, App
998 1.8 116 4 US-09-252-931A-26837 Sequence 26837, A
999 1.8 116 4 US-09-107-532A-6182 Sequence 6182, App
1000 1.8 117 1 US-08-262-037-58 Sequence 58, Appl

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ALIGNMENTS

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RESULT 1
US-09-385-028-11
; Sequence 11, Application US/09385028
; Patent No. 6232106
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paradkar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6232106
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: The Jennifer Building, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09385,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 39305350
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-385-028-11
Query Match 2.9%; Score 8; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 GKVALITG 20
Db 7 GKVALITG 14
RESULT 2
US-09-726-614-11
; Sequence 11, Application US/09726614
; Patent No. 6514735
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paradkar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6514735
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: The Jennifer Building, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09726,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 39305350
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-726-614-11
Query Match 2.9%; Score 8; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 GKVALITG 20
Db 7 GKVALITG 14
RESULT 3
US-09-328-352-5742
; Sequence 5742, Application US/09328352

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; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5742  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5742

Query Match 2.9%; Score 8; DB 4; Length 262;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KQUALITG 20  
| | | | |  
Db 18 GKVALITG 25

RESULT 4  
US-09-252-991A-19626  
; Sequence 19626, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19626  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19626

Query Match 2.9%; Score 8; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 IRVNCCLSP 192  
| | | | |  
Db 196 IRVNCCLSP 203

RESULT 5  
US-09-134-001C-4339  
; Sequence 4339, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4339  
; LENGTH: 290

; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4339  
Query Match 2.9%; Score 8; DB 4; Length 290;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITGG 21  
| | | | |  
Db 46 KVALITGG 53

RESULT 6  
US-09-026-482B-2  
; Sequence 2, Application US/09026482B  
; Patent No. 6143538  
; GENERAL INFORMATION:  
; APPLICANT: REISER, STEVEN E.  
; APPLICANT: SOMMERVILLE, CHRIS  
; TITLE OF INVENTION: ACYL-COA REDUCTASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PAUL A. GOTTLIEB, AGCTT  
; ADDRESSEE: DEPARTMENT OF ENERGY  
; ADDRESSEE: GC-62 (FORSTL) MS-6F-067  
; STREET: 1000 INDEPENDENCE AVE. S.W.  
; CITY: WASHINGTON, D.C.  
; ZIP: 20585  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORDPERFECT 6.22  
; CURRENT APPLICATION DATA: US/09/026,482B  
; APPLICATION NUMBER: 02/19/98  
; FILING DATE: 02/19/98  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ALWAN, JOY  
; REGISTRATION NUMBER: 40486  
; REFERENCE/DOCKET NUMBER: S-87814  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 630-252-2179  
; TELEFAX: 630-252-2779  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 295 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-026-482B-2

Query Match 2.9%; Score 8; DB 3; Length 295;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITG 20  
| | | | |  
Db 15 GKVALITG 22

RESULT 7  
US-08-580-545B-2  
; Sequence 2, Application US/08580545B  
; Patent No. 5932713  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihisa, Kasukabe  
; APPLICANT: Koichi, Fujisawa  
; APPLICANT: Susumu, Nishiguchi  
; APPLICANT: Yoshihiko, Maekawa  
; APPLICANT: Randy, Allen  
; TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES

NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 601 Thirteenth Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,545B  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Bretschneider, Barry E.  
REGISTRATION NUMBER: 28,055  
REFERENCE/DOCKET NUMBER: 04473/068001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/783-5070  
TELEFAX: 202/783-2331  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-545B-2

Query Match 2.9%; Score 8; DB 2; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 TGGASGIG 26  
Db 40 TGGASGIG 47

RESULT 8  
US-09-262-653A-2  
Sequence 2, Application US/09262653A  
Patent No. 6168294  
GENERAL INFORMATION:  
APPLICANT: Yoshihisa, Kasukabe  
APPLICANT: Koichi, Fujisawa  
APPLICANT: Susumu, Nishiguchi  
APPLICANT: Yoshihiko, Maekawa  
APPLICANT: Randy, Allen  
TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 601 Thirteenth Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/262,653A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Bretschneider, Barry E.  
REGISTRATION NUMBER: 28,055  
REFERENCE/DOCKET NUMBER: 04473/068001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/783-5070  
TELEFAX: 202/783-2331  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-262-653A-2

Query Match 2.9%; Score 8; DB 3; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 TGGASGIG 26  
Db 40 TGGASGIG 47

RESULT 9  
US-09-328-352-4279  
Sequence 4279, Application US/09328352  
Patent No. 6562358  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 4279  
LENGTH: 87  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-4279

Query Match 2.6%; Score 7; DB 4; Length 87;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 140 RSGNIIS 146  
Db 65 RSGNIIS 71

RESULT 10  
US-09-252-991A-21618  
Sequence 21618, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21618  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21618

Query Match 2.6%; Score 7; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 176 LAVELGQ 182  
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 Db 47 LAVELGQ 53

## RESULT 11

US-09-252-991A-18834  
 ; Sequence 18834, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252.991A  
 ; PRIOR FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 18834  
 ; LENGTH: 175  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-18834

Query Match 2.6%; Score 7; DB 4; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 ARVMIPA 139  
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 Db 108 ARVMIPA 114

## RESULT 12

US-09-648-004-20  
 ; Sequence 20, Application US/09648004  
 ; Patent No. 6498242  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHEN, QIONG  
 ; APPLICANT: THOMAS, STUART  
 ; APPLICANT: NAGARAJAN, VASANTHA  
 ; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
 ; TITLE OF INVENTION: INTERMEDIATES  
 ; FILE REFERENCE: CL-1341-A  
 ; CURRENT APPLICATION NUMBER: US/09/648.004  
 ; CURRENT FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 09/252,553  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 20  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter sp.  
 ; US-09-648-004-20

Query Match 2.6%; Score 7; DB 4; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITG 20  
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 Db 12 KVALITG 18

## RESULT 13

US-08-815-225-2  
 ; Sequence 2, Application US/08815225  
 ; Patent No. 6268479  
 ; GENERAL INFORMATION:

; APPLICANT: Stern, David M.  
 ; APPLICANT: Yan, Shi Du  
 ; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
 ; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING  
 ; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/815,225  
 ; FILING DATE: 12-MAR-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 0575/55209  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 261 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-815-225-2

Query Match 2.6%; Score 7; DB 3; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24  
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 Db 15 ITGGASG 21

## RESULT 14

US-08-815-225-3  
 ; Sequence 3, Application US/08815225  
 ; Patent No. 6268479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Yan, Shi Du  
 ; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
 ; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING  
 ; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/815,225  
 ; FILING DATE: 12-MAR-1997  
 ; CLASSIFICATION: 536

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; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-815-225-3

Query Match      2.6%; Score 7; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 15
US-09-347-878-50
; Sequence 50, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-347-878-50

Query Match      2.6%; Score 7; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
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Search completed: October 23, 2003, 13:06:08  
Job time : 51 secs



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584	6	2.2	148	15	US-10-015-868A-336	Sequence 336, App	657	6	2.2	235	9	US-09-925-301-1293	Sequence 1293, App
585	6	2.2	148	15	US-10-179-526-360	Sequence 360, App	658	6	2.2	238	15	US-10-156-761-12027	Sequence 12027, A
586	6	2.2	148	15	US-10-223-085-242	Sequence 242, App	659	6	2.2	239	11	US-09-934-455-134	Sequence 134, App
587	6	2.2	148	15	US-10-173-701-360	Sequence 360, App	660	6	2.2	239	15	US-10-295-403-146	Sequence 146, App
588	6	2.2	148	15	US-10-179-511-360	Sequence 360, App	661	6	2.2	239	16	US-10-278-536-204	Sequence 204, App
589	6	2.2	148	15	US-10-179-518-360	Sequence 360, App	662	6	2.2	241	15	US-10-102-806-610	Sequence 610, App
590	6	2.2	148	15	US-10-183-018-360	Sequence 360, App	663	6	2.2	242	11	US-09-880-748-1884	Sequence 1884, App
591	6	2.2	148	15	US-10-184-624-360	Sequence 360, App	664	6	2.2	244	9	US-09-815-242-10094	Sequence 10094, A
592	6	2.2	148	15	US-10-184-657-360	Sequence 360, App	665	6	2.2	244	9	US-09-815-242-10126	Sequence 10126, A
593	6	2.2	148	15	US-10-197-701-360	Sequence 360, App	666	6	2.2	244	11	US-09-815-242-13891	Sequence 13891, A
594	6	2.2	148	15	US-10-197-706-360	Sequence 360, App	667	6	2.2	244	12	US-09-849-092-13	Sequence 13, Appl1
595	6	2.2	148	15	US-10-201-857-360	Sequence 360, App	668	6	2.2	244	12	US-09-769-744A-50	Sequence 50, Appl1
596	6	2.2	148	15	US-10-202-413-360	Sequence 360, App	669	6	2.2	245	15	US-10-233-131-29	Sequence 29, Appl1
597	6	2.2	148	15	US-10-202-938-360	Sequence 360, App	670	6	2.2	245	9	US-09-796-089-9	Sequence 9, Appl1
598	6	2.2	148	15	US-10-202-940-360	Sequence 360, App	671	6	2.2	245	12	US-10-237-496-82	Sequence 82, Appl1
599	6	2.2	148	15	US-10-205-508-360	Sequence 360, App	672	6	2.2	245	12	US-10-242-074-82	Sequence 82, Appl1

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702	6	2.2	245	15	US-10-245-621-82	Sequence 82, Appl	775	245	15	US-10-243-810-82	Sequence 82, Appl
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704	6	2.2	245	15	US-10-245-033-82	Sequence 82, Appl	777	246	9	US-10-246-098-82	Sequence 82, Appl
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709	6	2.2	245	15	US-10-245-770-82	Sequence 82, Appl	782	253	9	US-09-815-242-13878	Sequence 13878, A
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711	6	2.2	245	15	US-10-246-976-82	Sequence 82, Appl	784	253	11	US-09-934-455-184	Sequence 184, App
712	6	2.2	245	15	US-10-243-320-82	Sequence 82, Appl	785	257	9	US-09-864-761-37608	Sequence 37608, A
713	6	2.2	245	15	US-10-242-743-82	Sequence 82, Appl	786	257	9	US-09-815-242-11706	Sequence 11706, A
714	6	2.2	245	15	US-10-242-845-82	Sequence 82, Appl	787	257	15	US-10-156-761-12528	Sequence 12528, A
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716	6	2.2	245	15	US-10-238-325-82	Sequence 82, Appl	789	261	10	US-09-971-536-74	Sequence 74, Appl
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718	6	2.2	245	15	US-10-238-411-82	Sequence 82, Appl	791	263	14	US-10-067-989-3	Sequence 3, Appl
719	6	2.2	245	15	US-10-243-124-82	Sequence 82, Appl	792	267	9	US-09-726-613-63	Sequence 63, Appl
720	6	2.2	245	15	US-10-243-425-82	Sequence 82, Appl	793	267	14	US-10-042-141-63	Sequence 63, Appl
721	6	2.2	245	15	US-10-243-446-82	Sequence 82, Appl	794	270	15	US-10-286-264-96	Sequence 96, Appl
722	6	2.2	245	15	US-10-245-874-82	Sequence 82, Appl	795	273	12	US-10-289-795-13	Sequence 13, Appl
723	6	2.2	245	15	US-10-242-653-82	Sequence 82, Appl	796	274	10	US-09-976-059-17	Sequence 17, Appl
724	6	2.2	245	15	US-10-243-167-82	Sequence 82, Appl	797	278	12	US-09-866-034-2	Sequence 2, Appl
725	6	2.2	245	15	US-10-243-388-82	Sequence 82, Appl	798	278	12	US-10-210-951-60	Sequence 60, Appl
726	6	2.2	245	15	US-10-244-947-82	Sequence 82, Appl	799	278	12	US-10-211-884-60	Sequence 60, Appl
727	6	2.2	245	15	US-10-244-968-82	Sequence 82, Appl	800	278	13	US-10-033-246-2	Sequence 2, Appl
728	6	2.2	245	15	US-10-244-990-82	Sequence 82, Appl	801	278	13	US-10-033-301-2	Sequence 2, Appl
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738	6	2.2	245	15	US-10-245-899-82	Sequence 82, Appl	811	279	10	US-09-738-626-3942	Sequence 3942, Ap
739	6	2.2	245	15	US-10-245-900-82	Sequence 82, Appl	812	282	12	US-10-032-585-7746	Sequence 7746, Ap
740	6	2.2	245	15	US-10-247-058-82	Sequence 82, Appl	813	286	9	US-09-815-242-5592	Sequence 5592, Ap
741	6	2.2	245	15	US-10-245-454-82	Sequence 82, Appl	814	286	11	US-09-910-600-14	Sequence 14, Appl
742	6	2.2	245	15	US-10-237-471-82	Sequence 82, Appl	815	286	15	US-10-106-698-5072	Sequence 5072, Ap
743	6	2.2	245	15	US-10-238-261-82	Sequence 82, Appl	816	288	9	US-09-216-393-341	Sequence 341, App
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745	6	2.2	245	15	US-10-241-860-82	Sequence 82, Appl	818	288	9		



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820	6	2.2	288	12	US-10-321-856-344	Sequence 344, App	893	6	2.2	336	12	US-10-199-672-182	Sequence 182, App
821	6	2.2	290	12	US-10-238-075-498	Sequence 498, App	894	6	2.2	336	12	US-10-187-749-182	Sequence 182, App
822	6	2.2	292	10	US-09-940-037A-2	Sequence 2, Appli	895	6	2.2	336	12	US-10-194-457-182	Sequence 182, App
823	6	2.2	292	10	US-09-738-626-5836	Sequence 5836, Ap	896	6	2.2	336	12	US-10-145-128A-303	Sequence 303, App
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825	6	2.2	294	15	US-10-128-714-3283	Sequence 3283, Ap	898	6	2.2	336	12	US-10-196-747-182	Sequence 182, App
826	6	2.2	295	9	US-09-815-242-11833	Sequence 11833, A	899	6	2.2	336	12	US-10-173-689-182	Sequence 182, App
827	6	2.2	296	10	US-09-940-037A-23	Sequence 23, Appl	900	6	2.2	336	12	US-10-173-690-182	Sequence 182, App
828	6	2.2	296	10	US-09-823-829-18	Sequence 18, Appl	901	6	2.2	336	12	US-10-173-691-182	Sequence 182, App
829	6	2.2	296	10	US-09-823-823-18	Sequence 18, Appl	902	6	2.2	336	12	US-10-173-692-182	Sequence 182, App
830	6	2.2	296	10	US-09-738-626-6533	Sequence 6533, Ap	903	6	2.2	336	12	US-10-173-694-182	Sequence 182, App
831	6	2.2	297	10	US-09-764-868-1162	Sequence 1162, Ap	904	6	2.2	336	12	US-10-173-698-182	Sequence 182, App
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835	6	2.2	309	15	US-10-156-761-11336	Sequence 11336, A	908	6	2.2	336	12	US-10-174-583-182	Sequence 182, App
836	6	2.2	310	9	US-09-815-242-10707	Sequence 10707, A	909	6	2.2	336	12	US-10-174-587-182	Sequence 182, App
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838	6	2.2	311	12	US-10-032-201B-211	Sequence 211, App	911	6	2.2	336	12	US-10-174-591-182	Sequence 182, App
839	6	2.2	312	10	US-09-761-640-8	Sequence 8, Appli	912	6	2.2	336	12	US-10-175-736-182	Sequence 182, App
840	6	2.2	312	12	US-10-024-806-4	Sequence 4, Appli	913	6	2.2	336	12	US-10-175-742-182	Sequence 182, App
841	6	2.2	312	15	US-10-156-761-11045	Sequence 11045, A	914	6	2.2	336	12	US-10-175-744-182	Sequence 182, App
842	6	2.2	314	9	US-09-841-132-521	Sequence 521, App	915	6	2.2	336	12	US-10-175-745-182	Sequence 182, App
843	6	2.2	314	12	US-10-306-762-92	Sequence 92, Appl	916	6	2.2	336	12	US-10-175-748-182	Sequence 182, App
844	6	2.2	315	12	US-10-032-201B-215	Sequence 215, App	917	6	2.2	336	12	US-10-174-591-182	Sequence 182, App
845	6	2.2	315	16	US-10-156-136-18	Sequence 18, Appl	918	6	2.2	336	12	US-10-175-751-182	Sequence 182, App
846	6	2.2	316	14	US-10-001-870-132	Sequence 132, App	919	6	2.2	336	12	US-10-175-754-182	Sequence 182, App
847	6	2.2	317	15	US-10-156-761-14831	Sequence 14831, A	920	6	2.2	336	12	US-10-176-480-182	Sequence 182, App
848	6	2.2	318	11	US-09-849-092-39	Sequence 39, Appl	921	6	2.2	336	12	US-10-176-489-182	Sequence 182, App
849	6	2.2	318	12	US-10-024-806-2	Sequence 2, Appli	922	6	2.2	336	12	US-10-176-754-182	Sequence 182, App
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851	6	2.2	320	12	US-10-024-806-6	Sequence 6, Appli	924	6	2.2	336	12	US-10-176-759-182	Sequence 182, App
852	6	2.2	323	9	US-09-815-242-11477	Sequence 11477, A	925	6	2.2	336	12	US-10-176-920-182	Sequence 182, App
853	6	2.2	325	10	US-09-886-055-233	Sequence 233, App	926	6	2.2	336	12	US-10-176-922-182	Sequence 182, App
854	6	2.2	325	11	US-09-804-291-233	Sequence 233, App	927	6	2.2	336	12	US-10-176-924-182	Sequence 182, App
855	6	2.2	325	12	US-10-017-161-102	Sequence 102, App	928	6	2.2	336	12	US-10-176-984-182	Sequence 182, App
856	6	2.2	326	12	US-10-138-701-53	Sequence 53, Appl	929	6	2.2	336	12	US-10-179-508-182	Sequence 182, App
857	6	2.2	326	15	US-10-245-538-4	Sequence 4, Appli	930	6	2.2	336	12	US-10-179-512-182	Sequence 182, App
858	6	2.2	326	15	US-10-156-761-9201	Sequence 9201, Ap	931	6	2.2	336	12	US-10-179-515-182	Sequence 182, App
859	6	2.2	326	15	US-10-156-761-12620	Sequence 12620, A	932	6	2.2	336	12	US-10-017-191A-303	Sequence 303, App
860	6	2.2	327	9	US-09-925-301-862	Sequence 862, App	933	6	2.2	336	12	US-10-173-702-182	Sequence 182, App
861	6	2.2	328	15	US-10-156-761-9776	Sequence 9776, Ap	934	6	2.2	336	12	US-10-173-703-182	Sequence 182, App
862	6	2.2	332	12	US-09-890-688-108	Sequence 108, App	935	6	2.2	336	12	US-10-173-704-182	Sequence 182, App
863	6	2.2	332	12	US-10-278-946-20	Sequence 20, Appl	936	6	2.2	336	12	US-10-174-574-182	Sequence 182, App
864	6	2.2	334	15	US-10-156-761-8246	Sequence 8246, Ap	937	6	2.2	336	12	US-10-176-486-182	Sequence 182, App
865	6	2.2	335	10	US-09-764-864-1178	Sequence 1178, Ap	938	6	2.2	336	12	US-10-176-490-182	Sequence 182, App
866	6	2.2	336	10	US-09-978-295A-303	Sequence 303, App	939	6	2.2	336	12	US-10-176-752-182	Sequence 182, App
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868	6	2.2	336	10	US-09-978-192A-303	Sequence 303, App	941	6	2.2	336	12	US-10-176-983-182	Sequence 182, App
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871	6	2.2	336	11	US-09-978-189-303	Sequence 303, App	944	6	2.2	336	12	US-10-179-521-182	Sequence 182, App
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875	6	2.2	336	11	US-09-978-403A-303	Sequence 303, App	948	6	2.2	336	12	US-10-202-475-182	Sequence 182, App
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877	6	2.2	336	11	US-09-999-833A-303	Sequence 303, App	950	6	2.2	336	12	US-10-145-017A-303	Sequence 303, App
878	6	2.2	336	11	US-09-981-915A-303	Sequence 303, App	951	6	2.2	336	12	US-10-145-017A-303	Sequence 303, App
879	6	2.2	336	11	US-09-978-824-303	Sequence 303, App	952	6	2.2	336	12	US-10-164-728A-303	Sequence 303, App
880	6	2.2	336	11	US-09-918-585A-303	Sequence 303, App	953	6	2.2	336	12	US-10-165-067A-303	Sequence 303, App
881	6	2.2	336	11	US-09-978-423A-303	Sequence 303, App	954	6	2.2	336	12	US-10-145-124A-303	Sequence 303, App
882	6	2.2	336	11	US-09-978-193A-303	Sequence 303, App	955	6	2.2	336	12	US-10-160-502A-303	Sequence 303, App
883	6	2.2	336	11	US-09-999-830A-303	Sequence 303, App	956	6	2.2	336	12	US-10-165-247A-303	Sequence 303, App
884	6	2.2	336	11	US-09-978-757A-303	Sequence 303, App	957	6	2.2	336	12	US-09-978-681A-303	Sequence 303, App
885	6	2.2	336	11	US-09-978-187B-303	Sequence 303, App	958	6	2.2	336	12	US-09-999-829A-303	Sequence 303, App
886	6	2.2	336	11	US-09-978-643A-303	Sequence 303, App	959	6	2.2	336	12	US-10-013-922A-303	Sequence 303, App
887	6	2.2	336	12	US-09-978-375A-303	Sequence 303, App	960	6	2.2	336	12	US-10-017-086A-303	Sequence 303, App
888	6	2.2	336	12	US-09-978-188A-303	Sequence 303, App	961	6	2.2	336	12	US-10-145-087A-303	Sequence 303, App
889	6	2.2	336	12	US-09-978-298A-303	Sequence 303, App	962	6	2.2	336	12	US-10-164-829A-303	Sequence 303, App
890	6	2.2	336	12	US-10-143-031A-303	Sequence 303, App	963	6	2.2	336	14	US-10-164-929A-303	Sequence 182, App
891	6	2.2	336	12	US-10-002-967A-303	Sequence 303, App	964	6	2.2	336	15	US-10-052-586-182	Sequence 182, App
892	6	2.2	336	12	US-10-017-083A-303	Sequence 303, App	964	6	2.2	336	15	US-10-174-590-182	Sequence 182, App

965 6 2.2 336 15 US-10-176-758-182 Sequence 182, App  
 966 6 2.2 336 15 US-10-176-737-182 Sequence 182, App  
 967 6 2.2 336 15 US-10-173-706-182 Sequence 182, App  
 968 6 2.2 336 15 US-10-173-738-182 Sequence 182, App  
 969 6 2.2 336 15 US-10-173-752-182 Sequence 182, App  
 970 6 2.2 336 15 US-10-176-482-182 Sequence 182, App  
 971 6 2.2 336 15 US-10-176-757-182 Sequence 182, App  
 972 6 2.2 336 15 US-10-176-913-182 Sequence 182, App  
 973 6 2.2 336 15 US-10-180-552-182 Sequence 182, App  
 974 6 2.2 336 15 US-10-180-557-182 Sequence 182, App  
 975 6 2.2 336 15 US-10-173-700-182 Sequence 182, App  
 976 6 2.2 336 15 US-10-174-572-182 Sequence 182, App  
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 978 6 2.2 336 15 US-10-174-588-182 Sequence 182, App  
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 980 6 2.2 336 15 US-10-175-739-182 Sequence 182, App  
 981 6 2.2 336 15 US-10-175-740-182 Sequence 182, App  
 982 6 2.2 336 15 US-10-175-743-182 Sequence 182, App  
 983 6 2.2 336 15 US-10-176-488-182 Sequence 182, App  
 984 6 2.2 336 15 US-10-176-492-182 Sequence 182, App  
 985 6 2.2 336 15 US-10-176-747-182 Sequence 182, App  
 986 6 2.2 336 15 US-10-176-750-182 Sequence 182, App  
 987 6 2.2 336 15 US-10-176-985-182 Sequence 182, App  
 988 6 2.2 336 15 US-10-176-987-182 Sequence 182, App  
 989 6 2.2 336 15 US-10-176-992-182 Sequence 182, App  
 990 6 2.2 336 15 US-10-176-993-182 Sequence 182, App  
 991 6 2.2 336 15 US-10-184-588-182 Sequence 182, App  
 992 6 2.2 336 15 US-10-176-991-182 Sequence 182, App  
 993 6 2.2 336 15 US-10-173-695-182 Sequence 182, App  
 994 6 2.2 336 15 US-10-173-697-182 Sequence 182, App  
 995 6 2.2 336 15 US-10-173-705-182 Sequence 182, App  
 996 6 2.2 336 15 US-10-174-576-182 Sequence 182, App  
 997 6 2.2 336 15 US-10-174-585-182 Sequence 182, App  
 998 6 2.2 336 15 US-10-174-586-182 Sequence 182, App  
 999 6 2.2 336 15 US-10-175-747-182 Sequence 182, App  
 1000 6 2.2 336 15 US-10-176-481-182 Sequence 182, App

ALIGNMENTS

RESULT 1  
 US-09-944-160-24  
 ; Sequence 24, Application US/09944160  
 ; Patent No. US20020174452A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lewis, No. US20020174452A1man  
 ; APPLICANT: Davin, Laurence  
 ; APPLICANT: .. Huang, Ning  
 ; TITLE OF INVENTION: Monocot Seeds with Increased Lignan  
 ; FILE REFERENCE: WSUR117983  
 ; CURRENT APPLICATION NUMBER: US/09/944,160  
 ; PRIOR FILING DATE: 2001-08-30  
 ; PRIOR FILING DATE: 2000-09-07  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 276  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: secisolaricresinol dehydrogenase amino acid  
 ; OTHER INFORMATION: sequence from plasmid pAPI249  
 US-09-944-160-24

Query Match 12.5%; Score 34; DB 10; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-25;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 SNSTYIHCDVTNEDGVKNAVDNTVSTYGLDIMP 93  
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Db 63 SNSTYIHCDVTNEDGVKNAVDNTVSTYGLDIMP 96  
 RESULT 2  
 US-10-156-761-14812  
 ; Sequence 14812, Application US/10156761  
 ; Publication No. US20030119018A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OMURA, SATOSHI  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIBA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; APPLICANT: HATTORI, MASAHIRA  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-262  
 ; CURRENT APPLICATION NUMBER: US/10/156,761  
 ; PRIOR FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2001-204089  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2001-272697  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 14812  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis  
 US-10-156-761-14812

Query Match 2.9%; Score 8; DB 15; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGASGIG 26  
 |||||  
 Db 12 TGGASGIG 19

RESULT 3  
 US-10-156-761-14537-  
 ; Sequence 14537, Application US/10156761  
 ; Publication No. US20030119018A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OMURA, SATOSHI  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIBA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; APPLICANT: HATTORI, MASAHIRA  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-262  
 ; CURRENT APPLICATION NUMBER: US/10/156,761  
 ; PRIOR FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2001-204089  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2001-272697  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 14537  
 ; LENGTH: 253  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis  
 US-10-156-761-14537

Query Match 2.9%; Score 8; DB 15; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GKVALITG 20  
 |||||  
 Db 9 GKVALITG 16

Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 4

US-09-815-242-10597  
; Sequence 10597, Application US/09815242  
; Patent No. US2002061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 10597  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis

Query Match 2.9%; Score 8; DB 9; Length 262;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITG 20  
| | | | | | | |  
Db 12 GKVALITG 19

## RESULT 5

US-10-238-075-473  
; Sequence 473, Application US/10238075  
; Publication No. US2003014832A1  
; GENERAL INFORMATION:  
; APPLICANT: I. N. S. E. R. M.  
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat  
; FILE REFERENCE: BLANDINE  
; CURRENT APPLICATION NUMBER: US/10/238,075  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 0003145  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 473  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Escherichia coli

Query Match 2.9%; Score 8; DB 12; Length 268;

Qy 19 TGGASGIG 26  
| | | | | | | |  
Db 15 TGGASGIG 22

## RESULT 6

US-09-984-245-128  
; Sequence 128, Application US/09984245  
; Patent No. US20020165374A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: P2004P1  
; CURRENT APPLICATION NUMBER: US/09/984,245  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/050,937  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,187  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,352  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,186  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,069  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,095  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,131  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,096  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,351  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,154  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/054,804  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: US 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: US 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 128

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;
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-128

Query Match          2.6%; Score 7; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 7
US-09-966-262-128
; Sequence 128, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
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;
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-128

Query Match          2.6%; Score 7; DB 11; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 8
US-09-983-966-128
; Sequence 128, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-128

Query Match          2.6%; Score 7; DB 11; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 9
US-10-143-090-128
; Sequence 128, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; .NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-090-128

Query Match          2.6%; Score 7; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 10
US-10-106-698-4341
; Sequence 4341, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 4341
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4341

Query Match          2.6%; Score 7; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GIGETTA 30
Db 80 GIGETTA 86

RESULT 11
US-10-291-190-45
; Sequence 45, Application US/10291190
; Publication No. US20030171549A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Park, Rfances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF YIIM PROTEINS
; FILE REFERENCE: 52498-20009.00
; CURRENT APPLICATION NUMBER: US/10/291,190
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/337,769
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 181
; TYPE: PRT
; ORGANISM: D. radiodurans (15806071)
US-10-291-190-45

Query Match          2.6%; Score 7; DB 12; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 RVLNVV 122
Db 2 RVLNVV 8

RESULT 12
US-09-815-242-13753
; Sequence 13753, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Hasebeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
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; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13753  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Salmonella typhi  
US-09-815-242-13753

Query Match 2.6%; Score 7; DB 9; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 PTALGKK 202  
Db 98 PTALGKK 104  
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RESULT 13  
US-09-811-284-144  
; Sequence 144, Application US/09811284  
; Patent No. US20020058306A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogell, Gabriel  
; TITLE OF INVENTION: No. US20020058306A1el G Protein-Coupled Receptors  
; FILE REFERENCE: 00167051  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/189,783  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/189,907  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/189,918  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/189,960  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/189,917  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/192,945  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/192,916  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/192,923  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/192,933  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/192,830  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/192,234  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/192,155  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,935  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 258  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 144  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-811-284-144

Query Match 2.6%; Score 7; DB 9; Length 204;

.Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 STASLSS 152  
Db 131 STASLSS 137  
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RESULT 14  
US-10-156-761-9390  
; Sequence 9390, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9390  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9390

Query Match 2.6%; Score 7; DB 15; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGG 21  
Db 6 VALITGG 12  
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RESULT 15  
US-10-272-419-20  
; Sequence 20, Application US/10272419  
; Publication No. US20030087403A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, QIONG  
; APPLICANT: THOMAS, STUART  
; APPLICANT: NAGARAJAN, VASANTHA  
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
; FILE REFERENCE: C11341-A  
; CURRENT APPLICATION NUMBER: US/10/272,419  
; CURRENT FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 09/252,553  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 20  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Acinetobacter sp.  
US-10-272-419-20

Query Match 2.6%; Score 7; DB 15; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITG 20  
|||||

Db 12 KVALITG 18

Search completed: October 23, 2003, 13:15:07  
Job time : 110 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: October 23, 2003, 12:59:30 ; Search time 40 Seconds  
(without alignments)  
656.351 Million cell updates/sec

Title: US-09-673-918a-2

Perfect score: 273

Sequence: 1 MQLRTAFARLEKGVALITG.....IDGGFVCNSVIKVFQYPS 273

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	6-2	234	2 T03734	short chain alcohol
2	17	6-2	284	2 T02257	probable short cha
3	16	5-9	283	2 H85039	probable alcohol d
4	13	4-8	267	2 T11579	probable short cha
5	10	3-7	255	1 S39737	glucose 1-dehydrog
6	10	3-7	255	2 C87434	2-deoxy-D-gluconat
7	10	3-7	256	2 AD2307	hypothetical prote
8	10	3-7	262	2 AB3545	toluenesulfonate z
9	10	3-7	285	2 F96563	hypothetical prote
10	9	3-3	15	2 PC4213	bphB protein - Com
11	9	3-3	245	2 B82680	pteridine reductas
12	9	3-3	257	2 T02175	probable alcohol d
13	9	3-3	258	2 T02176	probable alcohol d
14	9	3-3	258	2 H75616	oxidoreductase, sh
15	9	3-3	259	2 A13149	3-oxoacyl-(acyl-ca
16	9	3-3	259	2 H98137	3-oxoacyl-(acyl-ca
17	9	3-3	264	2 T02174	probable alcohol d
18	9	3-3	272	2 AC3359	glucose 1-dehydrog
19	9	3-3	275	2 C70814	hypothetical prote
20	9	3-3	286	2 D69768	alcohol dehydrogen
21	9	3-3	287	2 G83838	oxidoreductase (sh
22	9	3-3	288	2 C96590	hypothetical prote
23	9	3-3	303	2 T74064	short-chain alcohol
24	9	3-3	689	2 H70024	sorbitol-6-phospha
25	8	2-9	158	2 AD3301	2-deoxy-D-gluconat
26	8	2-9	240	2 H75014	3-oxoacyl-(acyl-ca
27	8	2-9	248	2 B97223	probable 3-ketoacy
28	8	2-9	252	2 B90495	hypothetical prote
29	8	2-9	253	1 S17711	probable dehydroge

30	8	2-9	254	2 E85069	hypothetical prote
31	8	2-9	256	2 B95274	probable oxidoredu
32	8	2-9	260	2 A84695	probable tropinone
33	8	2-9	262	2 B84695	probable tropinone
34	8	2-9	262	2 C84711	probable tropinone
35	8	2-9	285	2 D84643	probable ATP-depen
36	8	2-9	267	2 S50186	sorbitol-6-phospha
37	8	2-9	268	2 C91254	probable sorbitol-
38	8	2-9	268	2 G86094	D-glucitol-6-phosp
39	8	2-9	277	1 F42409	cis-2,3-dihydrobip
40	8	2-9	277	1 JN0814	cis-2,3-dihydrobip
41	8	2-9	277	2 JN0814	azarene carbazole
42	8	2-9	278	2 C75616	oxidoreductase, sh
43	8	2-9	279	2 T21410	hypothetical prote
44	8	2-9	285	2 AF2453	oxidoreductase alr
45	8	2-9	296	2 B87260	hypothetical prote
46	8	2-9	299	2 D97075	probable dehydroge
47	8	2-9	449	2 I40178	probable glutathio
48	8	2-9	629	2 D96533	ARP protein limpor
49	8	2-9	629	2 S57614	ARP protein - Arab
50	8	2-9	657	2 S77543	short-chain alcoho
51	7	2-6	111	2 H72707	hypothetical prote
52	7	2-6	133	2 T43374	ribosomal protein
53	7	2-6	136	2 T40638	60s ribosomal prot
54	7	2-6	141	2 G72661	hypothetical prote
55	7	2-6	146	2 A71115	hypothetical prote
56	7	2-6	153	2 A55139	myoglobin, body wa
57	7	2-6	154	2 T19332	hypothetical prote
58	7	2-6	159	2 B83245	hypothetical prote
59	7	2-6	167	1 F1SP5	photosystem I chai
60	7	2-6	172	2 B75338	thermoresistant gl
61	7	2-6	181	2 D75443	conserved hypoteth
62	7	2-6	188	2 AB0744	probable hydrolase
63	7	2-6	191	1 G69292	tryptophan repress
64	7	2-6	200	2 T02173	probable alcohol d
65	7	2-6	207	2 T32882	hypothetical prote
66	7	2-6	214	2 G70348	conserved hypoteth
67	7	2-6	215	2 T39928	probable transcrip
68	7	2-6	217	2 B83643	conserved hypoteth
69	7	2-6	231	2 S37778	filamin, muscle -
70	7	2-6	232	2 B82531	50S ribosomal prot
71	7	2-6	233	2 B90088	similar to proteas
72	7	2-6	243	2 AF3105	oxidoreductase Atu
73	7	2-6	245	2 AG3436	short-chain dehydr
74	7	2-6	246	2 AH0190	probable oxidoredu
75	7	2-6	248	2 F82128	3-oxoacyl-(acyl-ca
76	7	2-6	248	2 AF0177	probable beta-keto
77	7	2-6	248	2 AG3007	short-chain dehydr
78	7	2-6	248	2 G98276	short-chain dehydr
79	7	2-6	251	2 T06364	probable short-cha
80	7	2-6	252	2 E72612	hypothetical prote
81	7	2-6	255	2 T15987	hypothetical prote
82	7	2-6	255	2 D70635	hypothetical prote
83	7	2-6	255	2 S54515	probable membrane
84	7	2-6	257	2 AD2934	short chain dehydr
85	7	2-6	257	2 C98348	reductase (Al13282
86	7	2-6	261	2 B87279	hypothetical prote
87	7	2-6	261	2 E82748	hypothetical prote
88	7	2-6	261	2 AF2945	denhydrogenase Atu3
89	7	2-6	261	2 AG2810	short chain dehydr
90	7	2-6	261	2 B97589	1-2,3-butanediol d
91	7	2-6	261	2 D98337	L-iditol sorbitol d
92	7	2-6	264	2 F98181	oxidoreductase ucp
93	7	2-6	271	2 AE3150	dehydrogenase Atu4
94	7	2-6	271	2 D98137	2,5-dichloro-2,5-c
95	7	2-6	281	2 F69400	2-deoxy-D-gluconat
96	7	2-6	283	2 S41412	tetrahydroxynaphth
97	7	2-6	286	2 G83378	probable short-cha
98	7	2-6	295	2 S50729	sporulation protei
99	7	2-6	297	2 T09396	hypothetical prote
100	7	2-6	305	2 S35991	C-alpha-dehydrogen
101	7	2-6	323	2 AC2481	hypothetical prote
102	7	2-6	328	2 E83504	probable oxidoredu

103	7	2.6	328	2	E70695	probable oxidoreductase	176	6	2.2	87	2	I40094	hypothetical protein
104	7	2.6	339	2	S62596	ubiquinol-cytochrome c reductase	177	6	2.2	87	2	AC2740	ubiquinol-cytochrome c reductase
105	7	2.6	359	2	AG2212	hypothetical protein	178	6	2.2	87	2	AC2740	ubiquinol-cytochrome c reductase
106	7	2.6	362	2	AG3428	hypothetical protein	179	6	2.2	88	2	S36917	probable export protein
107	7	2.6	368	2	T20182	hypothetical protein	180	6	2.2	89	2	S78699	flagellar biosynthesis
108	7	2.6	372	2	G90983	GDP-mannose dehydratase	181	6	2.2	89	2	AE0753	probable outer membrane protein
109	7	2.6	372	2	B85829	GDP-mannose dehydratase	182	6	2.2	92	2	B90783	prophage pil protein
110	7	2.6	372	2	S28470	GDP-mannose 4,6-dehydrogenase	183	6	2.2	95	2	C86685	holin protein homolog
111	7	2.6	373	2	D64971	GDP-mannose dehydratase	184	6	2.2	95	2	T13259	probable signal recognition particle
112	7	2.6	373	2	B90986	GDP-mannose dehydratase	185	6	2.2	99	2	G75158	hypothetical protein
113	7	2.6	373	2	E85831	GDP-mannose dehydratase	186	6	2.2	99	2	G75158	hypothetical protein
114	7	2.6	373	2	AE0769	GDP-mannose 4,6-dehydrogenase	187	6	2.2	103	2	H72672	hypothetical protein
115	7	2.6	378	2	S44777	C30A5_3 protein	188	6	2.2	104	2	S75225	hypothetical protein
116	7	2.6	382	2	T23798	hypothetical protein	189	6	2.2	104	2	E72758	hypothetical protein
117	7	2.6	390	2	D84367	hypothetical protein	190	6	2.2	105	2	C71635	ribosomal protein
118	7	2.6	395	2	T06132	hypothetical protein	191	6	2.2	107	2	G72496	hypothetical protein
119	7	2.6	398	2	JC4254	ribosomal protein	192	6	2.2	110	2	B71524	hypothetical protein
120	7	2.6	399	2	AC2785	MSF permease (drug efflux)	193	6	2.2	118	2	D75580	hypothetical protein
121	7	2.6	400	2	D97564	protein C53B4_7 (fibrinogen-like)	194	6	2.2	119	2	S04521	histone H3 (clone)
122	7	2.6	414	2	D69895	conserved hypothetical protein	195	6	2.2	123	2	PT0387	conserved hypothetical protein
123	7	2.6	425	2	H90415	hypothetical protein	196	6	2.2	123	2	E81120	Ig heavy chain V region
124	7	2.6	431	2	G73305	hypothetical protein	197	6	2.2	135	2	G90363	probable periplasmic protein
125	7	2.6	441	2	H87587	hypothetical protein	198	6	2.2	135	2	C97946	conserved hypothetical protein
126	7	2.6	451	2	A85059	conserved hypothetical protein	199	6	2.2	136	2	F95078	conserved hypothetical protein
127	7	2.6	458	2	I33477	flagellin-specific	200	6	2.2	136	2	AF0356	holo-[acyl-carrier protein]
128	7	2.6	459	2	AH2426	glutathione-disulfide isomerase	201	6	2.2	136	2	E71925	cag island protein
129	7	2.6	466	2	H81697	amino acid antipporter	202	6	2.2	136	2	B82481	hypothetical protein
130	7	2.6	466	2	E84132	aminopeptidase BHI	203	6	2.2	136	2	D96518	hypothetical protein
131	7	2.6	475	2	T18487	hypothetical protein	204	6	2.2	136	2	F89989	hypothetical protein
132	7	2.6	502	2	AG3641	histidine-tRNA ligase	205	6	2.2	137	2	T04411	histone H3 - barle
133	7	2.6	515	2	F83891	spore germination	206	6	2.2	137	2	F69070	conserved hypothetical protein
134	7	2.6	559	2	AF0587	potassium-translocator	207	6	2.2	138	2	B44281	nucleoside diphosphate kinase
135	7	2.6	562	2	JC7709	testis-specific kinase	208	6	2.2	138	2	B44281	nucleoside diphosphate kinase
136	7	2.6	601	2	D83238	hypothetical protein	209	6	2.2	138	2	G71042	hypothetical protein
137	7	2.6	609	2	T52524	hypothetical protein	210	6	2.2	130	2	B72702	hypothetical protein
138	7	2.6	643	2	T03518	hypothetical protein	211	6	2.2	133	2	A72675	hypothetical protein
139	7	2.6	648	2	A49646	amine oxidase (cop)	212	6	2.2	133	2	F95323	hypothetical protein
140	7	2.6	724	2	AC2832	DNA ligase Atu2082	213	6	2.2	133	2	H72476	hypothetical protein
141	7	2.6	724	2	G97609	DNA ligase (polydeoxyribose)	214	6	2.2	134	2	A71136	hypothetical protein
142	7	2.6	737	1	S64767	probable serine/threonine kinase	215	6	2.2	134	2	AF2552	hypothetical protein
143	7	2.6	796	2	H90644	glucose dehydrogenase	216	6	2.2	136	2	S24346	hypothetical protein
144	7	2.6	796	2	H85495	glucose dehydrogenase	217	6	2.2	137	2	C86332	hypothetical protein
145	7	2.6	796	2	AG0523	glucose dehydrogenase	218	6	2.2	137	2	C69501	probable histone H3 protein
146	7	2.6	796	2	AG0523	glucose dehydrogenase	219	6	2.2	137	2	S22417	conserved hypothetical protein
147	7	2.6	797	2	AB3410	organic solvent tolerance	220	6	2.2	137	2	S74888	hypothetical protein
148	7	2.6	823	2	G90848	probable exonuclease	221	6	2.2	139	2	S22417	hypothetical protein
149	7	2.6	823	2	E85706	probable exonuclease	222	6	2.2	140	1	HABOKA	hemoglobin alpha chain
150	7	2.6	858	2	T03544	probable phospholipase	223	6	2.2	141	1	HABA1	hemoglobin alpha chain
151	7	2.6	858	2	A83424	CocC protein precursor	224	6	2.2	141	1	HABA1	hemoglobin alpha chain
152	7	2.6	908	2	S42874	assimilatory nitrate reductase	225	6	2.2	141	1	HABA1	hemoglobin alpha chain
153	7	2.6	934	1	S42874	oxoglutarate dehydrogenase	226	6	2.2	141	1	HABOG	hemoglobin alpha chain
154	7	2.6	942	2	S53963	MCS1 protein - yeast	227	6	2.2	142	2	B25727	hemoglobin alpha chain
155	7	2.6	976	2	T29583	hypothetical protein	228	6	2.2	142	2	B49141	hemoglobin alpha chain
156	7	2.6	1036	2	B69368	hypothetical protein	229	6	2.2	142	2	A58794	hemoglobin alpha chain
157	7	2.6	1107	2	S61667	probable membrane protein	230	6	2.2	142	2	T16898	hemoglobin alpha chain
158	7	2.6	1178	2	E82325	conserved hypothetical protein	231	6	2.2	143	2	T18166	hypothetical protein
159	7	2.6	1291	2	AF1116	internalin protein	232	6	2.2	143	2	T38240	40S ribosomal protein
160	7	2.6	1778	2	T37919	GCN1 homolog - fission yeast	233	6	2.2	143	2	T29740	hypothetical protein
161	6	2.2	2670	2	T37919	hypothetical protein	234	6	2.2	145	2	A46703	ribosomal protein
162	6	2.2	51	2	T28688	hypothetical protein	235	6	2.2	145	2	T00987	hypothetical protein
163	6	2.2	57	2	G72809	hypothetical protein	236	6	2.2	148	2	D64760	Yahr protein - E. coli
164	6	2.2	57	2	G72809	hypothetical protein	237	6	2.2	150	2	A87323	chemotaxis protein
165	6	2.2	61	2	G41476	probable antigen 7	238	6	2.2	150	2	H69514	hypothetical protein
166	6	2.2	62	2	B38309	histone H3.2 - alfalfa	239	6	2.2	152	2	G86303	hypothetical protein
167	6	2.2	66	2	H87791	hypothetical protein	240	6	2.2	152	2	AB2011	two-component response
168	6	2.2	72	2	B70517	hypothetical protein	241	6	2.2	158	2	S54083	hypothetical protein
169	6	2.2	74	2	JC4096	hypothetical protein	242	6	2.2	158	2	H83405	hypothetical protein
170	6	2.2	77	2	C97639	hypothetical protein	243	6	2.2	159	2	G84974	transcription elongation factor
171	6	2.2	80	1	H88H3	histone H3 - barle	244	6	2.2	159	2	H87539	conserved hypothetical protein
172	6	2.2	81	2	B84149	hypothetical protein	245	6	2.2	160	2	E71197	hypothetical protein
173	6	2.2	81	2	AG3596	transcription regulator	246	6	2.2	161	2	E48232	cysteine-rich protein
174	6	2.2	85	2	JC3290	hypothetical protein	247	6	2.2	161	2	AE1322	hypothetical protein
175	6	2.2	85	2	H83492	hypothetical protein	248	6	2.2	161	2	H88103	protein W10G1.4

249 6 2.2 162 2 G70005 hypothetical prote  
250 6 2.2 163 1 PRSAK staphylokinase - p  
251 6 2.2 163 2 S02330 staphylokinase - p  
252 6 2.2 163 2 G89983 STAPHYLOKINASE PRE  
253 6 2.2 164 2 T31280 benzoate 1,2-dioxy  
254 6 2.2 165 2 C42485 beta protein homol  
255 6 2.2 166 2 T49489 related to H+-tran  
256 6 2.2 167 1 S32716 ribosome releasing  
257 6 2.2 167 2 E83567 probable bacterioph  
258 6 2.2 167 2 D82448 hypothetical prote  
259 6 2.2 168 2 C82484 PPS system, IIA co  
260 6 2.2 168 2 J05132 contractile tube p  
261 6 2.2 168 2 T44546 hypothetical prote  
262 6 2.2 168 2 B96437 unknown protein [i  
263 6 2.2 168 2 C90209 hypothetical prote  
264 6 2.2 169 2 D82769 phage-related cont  
265 6 2.2 169 2 AF0039 probable regulator  
266 6 2.2 170 2 H84752 probable DOF zinc  
267 6 2.2 172 2 A71263 hypothetical prote  
268 6 2.2 174 2 T10075 periplasmic protei  
269 6 2.2 175 1 S74361 diacylglycerol kin  
270 6 2.2 175 2 T14775 hypothetical prote  
271 6 2.2 177 2 AH1613 modulates DNA topo  
272 6 2.2 178 2 T25432 hypothetical prote  
273 6 2.2 179 2 AE2225 hypothetical prote  
274 6 2.2 180 2 G64174 hypothetical prote  
275 6 2.2 180 2 T00116 hypothetical prote  
276 6 2.2 180 2 S65026 finger protein XFG  
277 6 2.2 180 2 AB3220 ECF family sigma f  
278 6 2.2 181 2 C95114 MutT/nudix family  
279 6 2.2 181 2 D97983 conserved hypoteth  
280 6 2.2 181 2 G71171 hypothetical prote  
281 6 2.2 185 2 AC3277 acetyltransferase  
282 6 2.2 185 2 T29117 hypothetical prote  
283 6 2.2 187 2 F69583 alkyl hydroperoxid  
284 6 2.2 188 2 C96593 unknown protein, 9  
285 6 2.2 189 2 T02792 hypothetical prote  
286 6 2.2 189 2 F82969 hypothetical prote  
287 6 2.2 191 2 G87253 hypothetical prote  
288 6 2.2 193 2 S37139 phenylalanine-tRNA  
289 6 2.2 194 2 AB2577 dephospho-CoA kin  
290 6 2.2 194 2 D97359 hypothetical prote  
291 6 2.2 194 2 T18336 iCM protein - Leg  
292 6 2.2 194 2 F97209 probable membrane  
293 6 2.2 195 2 G86683 prophage pil prote  
294 6 2.2 195 2 D90415 hypothetical prote  
295 6 2.2 196 2 A86690 prophage ps2 prote  
296 6 2.2 196 2 D84074 hypothetical prote  
297 6 2.2 197 2 AF0446 probable inhibitor  
298 6 2.2 200 2 AC0343 probable CDP-alcoh  
299 6 2.2 200 2 T40669 probable transcrip  
300 6 2.2 201 2 AH0288 glutathione transp  
301 6 2.2 201 2 D82896 hypothetical prote  
302 6 2.2 201 2 H82055 peptidyl-prolyl ci  
303 6 2.2 206 2 D83597 hypothetical prote  
304 6 2.2 209 2 AC0273 probable exported  
305 6 2.2 210 2 F71308 probable 2-dehydro  
306 6 2.2 211 2 D71306 probable adenylate  
307 6 2.2 211 2 S45464 hypothetical prote  
308 6 2.2 215 2 A95879 probable dihydroxy  
309 6 2.2 216 1 C41316 flagellin B2 precu  
310 6 2.2 216 2 B37332 transforming prote  
311 6 2.2 217 2 C70533 probable lexA prot  
312 6 2.2 218 1 B41316 flagellin B1 precu  
313 6 2.2 218 2 B47712 myelin/oligodendro  
314 6 2.2 219 2 B72662 hypothetical prote  
315 6 2.2 220 2 B84281 riboflavin-specifi  
316 6 2.2 220 2 JH0425 GRP-binding protei  
317 6 2.2 220 2 F72415 response regulator  
318 6 2.2 220 2 D71677 hypothetical prote  
319 6 2.2 221 2 G70533 probable phoY pro  
320 6 2.2 222 2 S19931 glycine-rich prote  
321 6 2.2 223 1 S72693 dethiobiotin synth

322 6 2.2 224 2 E83522 conserved hypoteth  
323 6 2.2 225 2 F84171 hypothetical prote  
324 6 2.2 225 2 F71439 probable serine pr  
325 6 2.2 226 2 B75270 ABC transporter, A  
326 6 2.2 226 2 D87061 dethiobiotin synth  
327 6 2.2 227 2 T15035 adenosylhomocyste  
328 6 2.2 228 2 F75493 hypothetical prote  
329 6 2.2 228 2 T49891 glycine-rich prote  
330 6 2.2 229 2 S73259 ribosomal protein  
331 6 2.2 229 2 E87328 ribosomal protein  
332 6 2.2 229 2 A97287 ribosomal protein  
333 6 2.2 229 2 AD3487 acylpruvate hydro  
334 6 2.2 231 1 S74852 orotidine 5', monoph  
335 6 2.2 231 2 AB3468 glycine betaine/l-  
336 6 2.2 233 2 T30747 hypothetical prote  
337 6 2.2 234 2 A84253 chemotaxis protein  
338 6 2.2 235 2 S72946 lexA protein - Myc  
339 6 2.2 235 2 E95876 conserved hypoteth  
340 6 2.2 236 2 A90190 hypothetical prote  
341 6 2.2 236 2 B96786 protein F10A5.19 [  
342 6 2.2 238 1 D69930 probable 3-oxoacyl  
343 6 2.2 238 2 F71723 ribosomal protein  
344 6 2.2 238 2 D71189 hypothetical prote  
345 6 2.2 239 2 E97722 50S ribosomal prot  
346 6 2.2 240 2 S77496 ribosomal protein  
347 6 2.2 240 2 G83208 conserved hypoteth  
348 6 2.2 240 2 H98031 hypothetical prote  
349 6 2.2 241 1 S06998 acetoacetyl-CoA re  
350 6 2.2 241 2 T17860 hypothetical prote  
351 6 2.2 242 2 C83882 phosphoesterase-re  
352 6 2.2 242 2 H86858 tRNA (guanine-2,  
353 6 2.2 244 1 B42147 3-oxoacyl-[acyl]-ca  
354 6 2.2 244 1 H64806 ybGL protein - Esc  
355 6 2.2 244 2 G90812 3-oxoacyl-[acyl]-ca  
356 6 2.2 244 2 C85672 3-oxoacyl-[acyl]-ca  
357 6 2.2 244 2 AD0642 3-oxoacyl-[acyl]-ca  
358 6 2.2 244 2 B95166 ABC transporter, A  
359 6 2.2 244 2 B90721 probable lactam ut  
360 6 2.2 244 2 H85571 conserved hypoteth  
361 6 2.2 244 2 AF0588 hypothetical prote  
362 6 2.2 244 2 S48482 hypothetical prote  
363 6 2.2 244 2 C75605 protein F53C3.4 [i  
364 6 2.2 244 2 B88115 nucleocapsid prote  
365 6 2.2 245 1 VHVUVV class II histocomp  
366 6 2.2 245 2 S29580 thif protein - Esc  
367 6 2.2 245 2 C65206 thiamin biosynthes  
368 6 2.2 245 2 C91243 thiamin biosynthes  
369 6 2.2 245 2 A86091 hypothetical prote  
370 6 2.2 245 2 E70583 hypothetical prote  
371 6 2.2 245 2 G81297 hypothetical prote  
372 6 2.2 245 2 C86418 3-oxoacyl-[acyl]-ca  
373 6 2.2 246 2 H84136 polyketide synthas  
374 6 2.2 246 2 JC5856 3-oxoacyl-[acyl]-ca  
375 6 2.2 246 2 H72219 3-oxoacyl-[acyl]-ca  
376 6 2.2 247 2 S77280 hypothetical oxido  
377 6 2.2 247 2 F65074 dihydroorotate deh  
378 6 2.2 247 2 D75027 oxoacyl (carrier p  
379 6 2.2 248 2 H86527 probable short-cha  
380 6 2.2 248 2 G83253 3-oxoacyl-[acyl]-ca  
381 6 2.2 248 2 D72096 oxidoreductase, sh  
382 6 2.2 249 1 A31841 bile acid dehydrog  
383 6 2.2 249 2 B96022 probable dehydroge  
384 6 2.2 249 2 A13573 undecaprenyl pyrop  
385 6 2.2 249 2 AD2180 hypothetical prote  
386 6 2.2 249 2 T11972 oxidoreductase, sh  
387 6 2.2 250 2 E82477 probable short-cha  
388 6 2.2 250 2 C83622 oxidoreductase, sh  
389 6 2.2 250 2 A70554 probable dehydroge  
390 6 2.2 251 2 G72389 3-oxoacyl-[acyl]-ca  
391 6 2.2 251 2 D69848 3-oxoacyl-[acyl]-ca  
392 6 2.2 251 2 AH2042 hypothetical prote  
393 6 2.2 251 2 T15495

395	6	2.2	252	2	D83766	3-oxoacyl-(acyl)-ca	468	2.2	268	2	AI2237	septum site-determ
396	6	2.2	252	2	F83098	probable short-cha	469	2.2	268	2	B64780	probable transport
397	6	2.2	252	2	H75123	thiamin biosynthet	470	2.2	268	2	B90698	probable metal res
398	6	2.2	252	2	AU0932	thiamin biosynthes	471	2.2	268	2	D85548	probable metal res
399	6	2.2	252	2	AE1985	HesA protein (impo	472	2.2	268	2	E82472	hypothetical prote
400	6	2.2	252	2	F72560	hypothetical prote	473	2.2	269	2	AE2285	glucose 1-dehydrag
401	6	2.2	252	2	H96965	short-chain dehydr	474	2.2	269	2	F97308	periplasmic amino
402	6	2.2	253	2	C85067	2-deoxy-D-gluconat	475	2.2	269	2	S74420	phosphate transpor
403	6	2.2	253	2	C91091	2-deoxy-D-gluconat	476	2.2	269	2	H71889	phosphomethylpyrim
404	6	2.2	253	2	B83332	cis-1,2-dihydroxyc	477	2.2	270	2	T00667	3-oxoacyl-(acyl)-ca
405	6	2.2	253	2	F83134	probable short-cha	478	2.2	270	2	S47479	outer surface prot
406	6	2.2	253	2	F85936	2-deoxy-D-gluconat	479	2.2	270	2	D64625	outer surface prot
407	6	2.2	253	2	B95284	probable (imported	480	2.2	272	2	E70879	thiamin biosynthes
408	6	2.2	253	2	AC0868	2-keto-3-deoxygluc	481	2.2	272	2	A97281	probable dehydroge
409	6	2.2	253	2	T27951	hypothetical prote	482	2.2	273	2	S71541	hydroxyethylthazo
410	6	2.2	253	2	T02106	hypothetical prote	483	2.2	273	2	S71544	outer surface prot
411	6	2.2	254	2	C70387	dehydrogenase - Ag	484	2.2	273	2	S71542	outer surface prot
412	6	2.2	254	2	S48129	3(or 17)beta-hydro	485	2.2	273	2	I40102	outer surface prot
413	6	2.2	254	2	AC3256	3-oxoacyl-(acyl)-ca	486	2.2	273	2	I40099	outer surface prot
414	6	2.2	254	2	AD3182	short chain dehydr	487	2.2	273	2	I40097	outer surface prot
415	6	2.2	254	2	S76646	hypothetical prote	488	2.2	273	2	I40139	outer surface prot
416	6	2.2	254	2	H69057	hypothetical prote	489	2.2	273	2	S71531	outer surface prot
417	6	2.2	254	2	F75540	probable histidine	490	2.2	273	2	S23112	outer surface prot
418	6	2.2	255	2	T33164	sorbitol utilization	491	2.2	274	2	B72227	nicotinate-nucleot
419	6	2.2	255	2	F71007	thiamin biosynthes	492	2.2	274	2	A64385	transketolase (EC
420	6	2.2	256	2	E72427	oxidoreductase, sh	493	2.2	275	2	B70640	hypothetical prote
421	6	2.2	256	2	D84201	enoyl-CoA hydratase	494	2.2	275	2	T01088	hypothetical prote
422	6	2.2	256	2	D87711	molybdopterin bios	495	2.2	276	2	D70953	hypothetical prote
423	6	2.2	257	2	D83280	probable short-cha	496	2.2	277	2	A43690	fdxH 5'-region hyp
424	6	2.2	257	2	T35593	probable dehydroge	497	2.2	277	2	S40167	hypothetical prote
425	6	2.2	257	2	D97152	uncharacterized se	498	2.2	277	2	S76356	proteinase IV (EC
426	6	2.2	257	2	T18754	hypothetical prote	499	2.2	277	2	E70878	hypothetical prote
427	6	2.2	258	2	T20484	hypothetical prote	500	2.2	278	1	SO1065	glutamine amidotra
428	6	2.2	258	2	T36264	probable dehydroge	501	2.2	278	1	AC0356	probable RpiR-fam
429	6	2.2	258	2	T09786	expansin - upland	502	2.2	279	2	D86658	oxidoreductase ycg
430	6	2.2	258	2	B83220	ferredoxin-NADP+ r	503	2.2	281	2	F97844	transcription regu
431	6	2.2	258	2	AS7432	ferredoxin-NADP re	504	2.2	281	2	AI3196	hypothetical prote
432	6	2.2	259	2	E55217	cis-1,2-dihydro-1,	505	2.2	281	2	T01445	hypothetical prote
433	6	2.2	259	2	D49343	cis-1,2-dihydro-1,	506	2.2	282	1	JC4041	D-arabinitol 2-deh
434	6	2.2	259	2	AE3185	dehydrogenase Atu5	507	2.2	282	2	T37144	probable oxidoredu
435	6	2.2	259	2	AB0565	probable membrane	508	2.2	282	2	D72771	probable bacterioc
436	6	2.2	259	2	AD2926	conserved hypoteth	509	2.2	283	2	S53941	hypothetical prote
437	6	2.2	259	2	C98356	hypothetical prote	510	2.2	284	2	T33860	hypothetical prote
438	6	2.2	260	2	C87264	3-hydroxyacyl-CoA	511	2.2	284	2	T50932	short-chain dehydr
439	6	2.2	260	2	H70758	probable fabG3 pro	512	2.2	285	2	D69835	alcohol dehydrogen
440	6	2.2	260	2	D62004	probable 3-oxoacyl	513	2.2	285	2	T51576	hypothetical prote
441	6	2.2	261	2	T38157	short-chain dehydr	514	2.2	285	1	A71090	hypothetical prote
442	6	2.2	261	2	AD2895	short-chain dehydr	515	2.2	286	2	A70667	hypothetical prote
443	6	2.2	261	2	G97670	probable oxidoredu	516	2.2	286	2	AI3207	NAD/NADP depend
444	6	2.2	262	2	G84694	probable tropinone	517	2.2	286	2	AG5193	dehydrogenase Atu5
445	6	2.2	262	2	T31253	1,6-dihydroxycyclo	518	2.2	287	2	AF2716	conserved hypoteth
446	6	2.2	262	2	F87498	exodeoxyribonuclea	519	2.2	287	2	S74895	hypothetical prote
447	6	2.2	262	2	AD0164	conserved hypoteth	520	2.2	288	2	T48108	hypothetical prote
448	6	2.2	263	2	S73266	ribosomal protein	521	2.2	289	2	D81738	hypothetical prote
449	6	2.2	263	2	B83751	N-acetylmuramoyl-L	522	2.2	290	1	F71901	probable 3',5'-cyc
450	6	2.2	263	2	A75280	phenylacetic acid	523	2.2	292	2	E64614	hypothetical prote
451	6	2.2	263	2	G97198	HAD superfamily hy	524	2.2	292	2	S35983	beta-alanine synth
452	6	2.2	264	2	T30224	3-oxoacyl-(acyl) ca	525	2.2	293	2	C90032	proline transport
453	6	2.2	264	2	S60874	phosphorylation-ac	526	2.2	293	2	T36063	hypothetical prote
454	6	2.2	264	2	F96832	hypothetical prote	527	2.2	293	2	C71703	probable integral
455	6	2.2	264	2	B72411	conserved hypoteth	528	2.2	294	2	AE1517	hypothetical prote
456	6	2.2	265	1	WMBE97	gene 7 protein - p	529	2.2	294	2	AB1158	oxidoreductase hom
457	6	2.2	265	2	S73294	hypothetical prote	530	2.2	294	2	H83452	probable short-cha
458	6	2.2	265	2	S70247	hypothetical prote	531	2.2	295	2	T51084	3-oxoacyl-(acyl)-ca
459	6	2.2	265	2	AE0455	thiamin biosynthes	532	2.2	297	2	S19842	probable oxidoredu
460	6	2.2	265	2	AE2964	transcription regu	533	2.2	297	2	AI1325	oxidoreductase Atu
461	6	2.2	265	2	H98318	hypothetical prote	534	2.2	298	2	AF1089	probable oxidoredu
462	6	2.2	266	2	T31264	cis-1,2-dihydro-1,	535	2.2	298	2	AF1578	transporter dme f
463	6	2.2	266	2	S78570	hypothetical prote	536	2.2	299	2	D81399	malate dehydrogena
464	6	2.2	266	2	S11900	hypothetical prote	537	2.2	300	2	C70586	probable bex Myc
465	6	2.2	267	1	F64103	suppressor protein	538	2.2	300	2	AC1597	integrase/recombin
466	6	2.2	268	2	AD2604	oxidoreductase Xf2	539	2.2	300	2	AE1234	
467	6	2.2	268	2	G96016	probable gluconate	540	2.2	300	2		

541	6	2.2	300	2	F81331	hypothetical prote	614	2	I39563	probable UDPglucos
542	6	2.2	302	2	A86898	phosphogluconate d	615	2	AB2772	inosine-uridine pr
543	6	2.2	302	2	T03575	conserved hypothet	616	2	S48698	3-dehydroquininate d
544	6	2.2	302	2	AH1749	transcription regu	617	6	C95952	hypothetical prote
545	6	2.2	302	2	D70538	transcription regu	618	6	B82301	conserved hypothet
546	6	2.2	303	2	H97014	transcription regu	619	6	G96812	protein F3P5.6 lim
547	6	2.2	304	2	F84298	cysteine synthase	620	6	YWBSF	protein F3P5.6 lim
548	6	2.2	304	2	T48281	hypothetical prote	621	6	F90675	probable sugar-bin
549	6	2.2	305	2	E89771	lipoprotein [impor	622	6	A85526	probable sugar-bin
550	6	2.2	306	2	S60670	ParA-like partitio	623	6	D71887	ADPglyceromanno-he
551	6	2.2	307	2	D75070	dipeptidase PA8238	624	6	YWBS	ADPglyceromanno-he
552	6	2.2	307	2	G95901	UDP-glucose 4-epim	625	6	C64827	tryptophan-tRNA li
553	6	2.2	308	2	D83452	probable cytochrom	626	6	F84008	ADPglyceromanno-he
554	6	2.2	308	2	A86378	protein F21J9.2 [i	627	6	A82510	tryptophanyl-tRNA
555	6	2.2	308	2	S67657	hypothetical prote	628	6	AG3650	conserved hypothet
556	6	2.2	308	2	G98161	hypothetical prote	629	6	AF1349	succinoglycan bios
557	6	2.2	308	2	AF2890	hypothetical oxido	630	6	AF11719	tryptophanyl-tRNA
558	6	2.2	308	2	B97666	transcription regu	631	6	A99605	tryptophanyl-tRNA
559	6	2.2	308	2	D70875	probable transcrip	632	6	A70388	hypothetical prote
560	6	2.2	308	2	T08798	probable PE protei	633	6	T39657	hydrogenase expre
561	6	2.2	309	2	C83136	hypothetical prote	634	6	A57140	hypothetical prote
562	6	2.2	309	2	B86702	probable epimerase	635	6	A49338	motB protein homol
563	6	2.2	309	2	F72316	Hpr(Ser) kinase [i	636	6	F69495	phosphate acetyltr
564	6	2.2	309	2	A83325	hypothetical prote	637	6	T05230	conserved hypothet
565	6	2.2	309	2	S67196	comL, competence l	638	6	AB1965	hypothetical prote
566	6	2.2	310	1	G70330	probable membrane	639	6	AF3309	tryptophanyl-tRNA
567	6	2.2	310	2	S45919	ADPglyceromanno-he	640	6	T26160	moXR protein [impo
568	6	2.2	311	1	A64623	hypothetical prote	641	6	G83207	hypothetical prote
569	6	2.2	311	2	T37155	thioredoxin-disulf	642	6	AE2922	hypothetical prote
570	6	2.2	311	2	T71890	probable oxidoredu	643	6	F97696	zinc-binding dehyd
571	6	2.2	311	2	A87527	thioredoxin reduct	644	6	A47542	hypothetical zinc-
572	6	2.2	311	2	T21206	ornithine carbamoy	645	6	H75255	short-chain alcoh
573	6	2.2	311	2	AP2810	hypothetical prote	646	6	T41543	oxidoreductase, sh
574	6	2.2	312	2	C96651	transcription regu	647	6	S77630	probable cell cycl
575	6	2.2	313	2	C81288	UDP-glucose 4-epim	648	6	TVMSFB	hypothetical prote
576	6	2.2	314	2	B70569	probable sugar-nuc	649	6	S48299	transforming prote
577	6	2.2	314	2	G86515	hypothetical prote	650	6	S73775	SAS2 protein - yea
578	6	2.2	314	2	E72107	oligopeptide perme	651	6	G82545	phage-related inte
579	6	2.2	314	2	D87576	peptide ABC transp	652	6	AF2018	hypothetical prote
580	6	2.2	314	2	A87693	oxidoreductase, al	653	6	F75557	hypothetical prote
581	6	2.2	314	2	S15311	transcription regu	654	6	D72025	oxidoreductase, sh
582	6	2.2	314	2	AI0765	hypothetical prote	655	6	B86598	flagellar m-ring p
583	6	2.2	315	1	S73917	probable rhamnosyl	656	6	AG2772	flagellar M-ring p
584	6	2.2	315	2	S39727	thioredoxin-disulf	657	6	E97552	NADPH:quinone redu
585	6	2.2	315	2	G96997	UDP-glucose 4,6-de	658	6	S60386	alcohol dehydrogen
586	6	2.2	315	2	E71729	nucleoside-diphosp	659	6	T41498	hypothetical prote
587	6	2.2	315	2	T00528	proteinase DO (htr	660	6	T22541	DNA (apurinic or a
588	6	2.2	316	1	S27981	hypothetical prote	661	6	AB3105	hypothetical prote
589	6	2.2	316	1	A42935	homoserine kinase	662	6	A98182	transcription regu
590	6	2.2	316	2	A38265	N-acetylmuramoyl-L	663	6	AB3105	transcription regu
591	6	2.2	316	2	H82958	peroxidase (EC 1.1	664	6	PC4185	electron transfer
592	6	2.2	317	1	S67781	homoserine kinase	665	6	B71296	hemagglutinin 1 ch
593	6	2.2	317	2	C86479	probable membrane	666	6	S36080	probable sn-1,2-di
594	6	2.2	318	2	E90541	probable annexin p	667	6	AB3105	hemagglutinin - in
595	6	2.2	318	2	G84196	hypothetical prote	668	6	AB3105	hemagglutinin 1 -
596	6	2.2	318	2	S56523	cation antiporter	669	6	AB3105	hemagglutinin 1 -
597	6	2.2	319	1	S56523	dihydrodipicolinat	670	6	AB3105	hemagglutinin 1 -
598	6	2.2	319	2	S22416	3-oxoacyl-[acyl-ca	671	6	AB3105	hemagglutinin 1 -
599	6	2.2	319	2	C89859	hypothetical prote	672	6	AB3105	hemagglutinin 1 -
600	6	2.2	319	2	D71633	[acyl-carrier-prot	673	6	AB3105	hemagglutinin 1 -
601	6	2.2	320	2	A97589	transcription regu	674	6	AB3105	hemagglutinin 1 -
602	6	2.2	320	2	S22450	3-oxoacyl-[acyl-ca	675	6	AB3105	hemagglutinin 1 -
603	6	2.2	320	2	AD1317	asparaginase homol	676	6	AB3105	hemagglutinin 1 -
604	6	2.2	320	2	AD1689	asparaginase homol	677	6	AB3105	hemagglutinin 1 -
605	6	2.2	320	2	B99254	formate hydrogenly	678	6	AB3105	hemagglutinin 1 -
606	6	2.2	321	2	G95920	probable epimerase	679	6	AB3105	hemagglutinin 1 -
607	6	2.2	322	2	S18999	asparaginase (EC 3	680	6	AB3105	hemagglutinin 1 -
608	6	2.2	322	2	JN0265	genome polyprotein	681	6	AB3105	hemagglutinin 1 -
609	6	2.2	323	2	A64470	NADH dehydrogenase	682	6	AB3105	hemagglutinin 1 -
610	6	2.2	323	2	T52563	probable DNA-(apur	683	6	AB3105	hemagglutinin 1 -
611	6	2.2	323	2	H71968	delta-aminolevulin	684	6	AB3105	hemagglutinin 1 -
612	6	2.2	323	2	D89773	hypothetical prote	685	6	AB3105	hemagglutinin 1 -
613	6	2.2	323	2	B48067	ethanolamine-phosp	686	6	AB3105	probable membrane

687	6	2.2	348	2	A70311	hypothenical prote	760	6	2.2	380	2	S78342	hypothenical prote
688	6	2.2	349	2	T41497	DNA (apurinic or a	761	6	2.2	380	2	G69604	spore coat protein
689	6	2.2	349	2	F95887	probable ABC trans	762	6	2.2	381	1	A42952	methanol dehydroge
690	6	2.2	349	2	A72605	probable high-affi	763	6	2.2	382	2	T11138	ubiquinol-cytochro
691	6	2.2	350	2	G75212	hypothenical prote	764	6	2.2	382	2	T49077	hypothenical prote
692	6	2.2	351	2	A11393	threonine synthase	765	6	2.2	382	2	T24963	hypothenical prote
693	6	2.2	351	2	A01768	threonine synthase	766	6	2.2	383	2	AG3229	NAD/NADP octopine/
694	6	2.2	351	2	A84827	hypothenical prote	767	6	2.2	384	2	S77238	hypothenical prote
695	6	2.2	351	2	F32880	hypothenical prote	768	6	2.2	384	2	S77238	probable coenzyme
696	6	2.2	351	2	F32880	hypothenical prote	769	6	2.2	385	2	A44102	di-N-acetylchitobi
697	6	2.2	353	1	HN1V8A	outer membrane prec	770	6	2.2	385	2	T09086	sedoheptulose-bisph
698	6	2.2	353	2	H34187	hypothenical prote	771	6	2.2	387	2	T23086	hypothenical prote
699	6	2.2	353	2	H69835	hypothenical prote	772	6	2.2	387	2	T23086	hypothenical prote
700	6	2.2	353	2	S50086	finger protein xpo	773	6	2.2	387	2	AE2750	hypothenical prote
701	6	2.2	354	1	F36397	probable X-Pro dip	774	6	2.2	388	1	D97531	ubiquinol-cytochro
702	6	2.2	354	2	F43245	aspartate-semialde	775	6	2.2	388	1	EA1339	xylose isomerase (
703	6	2.2	354	2	S46245	RAE-30 protein - m	776	6	2.2	388	2	JC1031	xylose isomerase (
704	6	2.2	355	2	G65182	dtDP-glucose 4,6-de	777	6	2.2	389	2	S01371	myosin heavy chain
705	6	2.2	355	2	A31219	dtDP-glucose 4,6-de	778	6	2.2	389	2	D84068	RNA helicase BH34
706	6	2.2	355	2	C86065	dtDP-glucose 4,6-de	779	6	2.2	389	2	F86212	hypothenical prote
707	6	2.2	355	2	C751134	x-pro aminopeptida	780	6	2.2	390	2	G75591	hypothenical prote
708	6	2.2	355	2	D97339	dioxygenase relate	781	6	2.2	391	2	T41849	oxidoreductase, sh
709	6	2.2	356	2	A91811	dtDP-glucose 4-6-d	782	6	2.2	391	2	A95979	ACMNPV orf109 - B
710	6	2.2	356	2	C97158	aminopeptidase P A	783	6	2.2	392	1	CBVF	probable sugar upt
711	6	2.2	356	2	A95361	probable transcrip	784	6	2.2	392	2	T36967	ubiquinol-cytochro
712	6	2.2	357	2	A31139	zinc-binding dehyd	785	6	2.2	393	1	S38960	probable geranylge
713	6	2.2	357	2	T08642	hypothenical prote	786	6	2.2	393	1	S38960	ubiquinol-cytochro
714	6	2.2	357	2	H65041	hypothenical prote	787	6	2.2	393	1	CBPOM	ubiquinol-cytochro
715	6	2.2	358	2	T05081	fructose-bisphosph	788	6	2.2	393	2	G71173	hypothenical prote
716	6	2.2	359	2	S83355	hypothenical prote	789	6	2.2	394	1	CBOBE	ubiquinol-cytochro
717	6	2.2	360	2	D93025	pleiotropic regula	790	6	2.2	395	2	F81343	probable integrat
718	6	2.2	361	2	S45299	dtDP-glucose 4,6-de	791	6	2.2	395	2	S70912	CMP-N-acetylneuram
719	6	2.2	361	2	A07667	dtDP-glucose 4,6-de	792	6	2.2	396	2	T11981	hypothenical prote
720	6	2.2	361	2	G72636	hypothenical prote	793	6	2.2	397	2	CBR2	ubiquinol-cytochro
721	6	2.2	361	2	A86393	hypothenical prote	794	6	2.2	397	2	T98148	(R,R)-butanediol d
722	6	2.2	362	2	E83542	tiK7.4 protein - A	795	6	2.2	397	2	A30091	caps protein - Bac
723	6	2.2	363	2	A33609	hypothenical prote	796	6	2.2	398	1	A22931	ubiquinol-cytochro
724	6	2.2	363	2	A33609	ABC transporter su	797	6	2.2	398	2	T49098	hypothenical prote
725	6	2.2	364	2	T45253	probable antipor	798	6	2.2	398	2	T08716	uracil permease -
726	6	2.2	365	1	AJFF32C	membrane fusion pr	799	6	2.2	399	2	F72329	hypothenical prote
727	6	2.2	365	2	A02090	NADH flavin oxidor	800	6	2.2	399	2	D86322	conserved hypotet
728	6	2.2	366	2	G82069	conserved hypotet	801	6	2.2	399	2	A95200	hypothenical prote
729	6	2.2	367	2	JC6138	extracellular sign	802	6	2.2	399	2	H98066	acetyl-CoA synthet
730	6	2.2	367	2	JC5252	mitogen-activated	803	6	2.2	400	2	B69081	tyrosine-tRNA liga
731	6	2.2	367	2	B41669	molybdenum cofacto	804	6	2.2	401	2	A81335	major capsid-like
732	6	2.2	368	2	E71204	hypothenical prote	805	6	2.2	401	2	T17500	renin-binding prot
733	6	2.2	368	2	A90539	hypothenical prote	806	6	2.2	402	2	A35741	hypothenical prote
734	6	2.2	369	2	T45021	Protein-Glutamate	807	6	2.2	402	2	D72400	hypothenical prote
735	6	2.2	371	2	A87322	Pentapeptide repea	808	6	2.2	402	2	T15677	nevalonate kinase
736	6	2.2	372	2	F01500	mannose-6-phosphat	809	6	2.2	404	1	S62440	probable valine-by
737	6	2.2	372	2	S67770	probable membrane	810	6	2.2	404	2	T36254	calreticulin precu
738	6	2.2	373	2	B95871	probable CUP-tyvel	811	6	2.2	405	1	JH0795	threonine synthase
739	6	2.2	373	2	A70334	hypothenical prote	812	6	2.2	405	2	H64482	probable flavoprot
740	6	2.2	374	2	D83328	probable aminotran	813	6	2.2	405	2	F97340	hypothenical prote
741	6	2.2	374	2	JC2124	major allergen Cry	814	6	2.2	405	2	S23260	aminotransferase n
742	6	2.2	374	2	JC2123	major allergen Cry	815	6	2.2	406	2	H64925	selenocysteine lya
743	6	2.2	374	2	B86198	hypothenical prote	816	6	2.2	406	2	C90927	selenocysteine lya
744	6	2.2	375	2	AC0484	probable regulator	817	6	2.2	406	2	G85775	probable aminotran
745	6	2.2	375	2	AC0484	flagella-associate	818	6	2.2	406	2	AG0702	hypothenical prote
746	6	2.2	376	2	E83954	actin - Cryptospor	819	6	2.2	407	2	C64250	tyrosine-tRNA liga
747	6	2.2	376	2	A45634	hypothenical prote	820	6	2.2	407	2	C64250	glutamate permease
748	6	2.2	377	1	D69027	conserved hypotet	821	6	2.2	408	2	B64708	hypothenical prote
749	6	2.2	377	2	S77142	tryptophan-tRNA li	822	6	2.2	409	2	T46063	glutamate permease
750	6	2.2	377	2	F91222	conserved hypotet	823	6	2.2	409	2	B95372	probable integrase
751	6	2.2	377	2	T45784	hypothenical prote	824	6	2.2	409	2	F95409	probable integrase
752	6	2.2	377	2	S6081	probable carrier p	825	6	2.2	410	2	T25165	two component sens
753	6	2.2	378	2	S11738	hemagglutinin prec	826	6	2.2	411	2	AE1052	hypothenical prote
754	6	2.2	378	2	A97552	chain a, crystal s	827	6	2.2	412	2	G64685	ammonium transport
755	6	2.2	378	2	AC0646	spermidine/putresc	828	6	2.2	413	2	H66823	conserved hypotet
756	6	2.2	378	2	AC0646	hypothenical prote	829	6	2.2	414	2	G82705	probable MFS trans
757	6	2.2	378	2	AH2104	synaptic vesicle m	830	6	2.2	415	2	C83544	transcobalamin i p
758	6	2.2	379	2	JN0013	conserved hypotet	831	6	2.2	416	2	S09334	conserved hypotet
759	6	2.2	379	2	B95883		832	6	2.2	417	2	F70132	

833	6	2.2	417	2	JX0188	renin-binding prot	906	2.2	472	2	F81208	glutamate-ammonia
834	6	2.2	417	2	B40016	matrin 3 - human (	907	2.2	472	2	H96607	unknown protein F2
835	6	2.2	417	2	F98233	two-component sens	908	2.2	474	2	T44424	dihydrolipoamide d
836	6	2.2	418	2	D83902	maltose/maltodextr	909	2.2	474	2	S30227	transposase - C10s
837	6	2.2	419	2	JX0187	renin-binding prot	910	2.2	475	2	C97684	2-isopropylmalate
838	6	2.2	419	2	A36509	N-acetylneuraminate	911	2.2	476	2	S12461	carboxypeptidase E
839	6	2.2	419	2	S53374	mannanase A - Pseu	912	2.2	476	2	A40469	carboxypeptidase E
840	6	2.2	419	2	D82408	conserved hypothet	913	2.2	476	2	S09489	carboxypeptidase E
841	6	2.2	421	2	T70038	maltose/maltodextr	914	2.2	476	2	F87324	hypothetical prote
842	6	2.2	421	2	E83038	probable heat-shoc	915	2.2	477	2	S16383	carboxypeptidase E
843	6	2.2	421	2	T19203	hypothetical prote	916	2.2	477	2	H83389	hypothetical prote
844	6	2.2	423	2	E84751	hypothetical prote	917	2.2	478	2	A45796	dihydrolipoamide d
845	6	2.2	425	2	G75414	seryl-tRNA synthet	918	2.2	478	2	A83449	dihydrolipoamide d
846	6	2.2	426	2	C97797	tetrahydrofolylpol	919	2.2	479	2	A48565	phosphogluconate d
847	6	2.2	427	2	T29376	hypothetical prote	920	2.2	479	2	T29720	hypothetical prote
848	6	2.2	427	2	A11491	permeases homolog	921	2.2	480	2	F86207	hypothetical prote
849	6	2.2	429	2	F71651	putrescine-ornithi	922	2.2	480	2	H70854	hypothetical prote
850	6	2.2	429	2	T40112	3-hydroxyisobutyry	923	2.2	481	2	S69808	lincomycin resist
851	6	2.2	432	2	A12613	hypothetical prote	924	2.2	481	2	T33733	hypothetical prote
852	6	2.2	432	2	G97395	hypothetical prote	925	2.2	483	2	T52136	dihydrolipoamide S
853	6	2.2	432	2	B75638	hypothetical prote	926	2.2	483	2	D87543	methionyl-CoA
854	6	2.2	433	1	A34227	transcobalamin I p	927	2.2	484	2	H64105	pantothenate trans
855	6	2.2	433	2	T46528	probable CDP-4-ket	928	2.2	484	2	T26393	hypothetical prote
856	6	2.2	433	2	G71657	folypolyglutamate	929	2.2	485	2	B82558	IMP dehydrogenase
857	6	2.2	433	2	C83271	conserved hypothet	930	2.2	485	2	H87463	hypothetical prote
858	6	2.2	438	2	A83544	probable transport	931	2.2	488	2	A72554	probable Glu-tRNA
859	6	2.2	438	2	G87337	membrane protein,	932	2.2	489	2	B72518	hypothetical prote
860	6	2.2	440	2	A21395	conserved hypothet	933	2.2	490	1	C57150	NADP-reducing hydr
861	6	2.2	440	2	A11770	conserved hypothet	934	2.2	492	2	T38211	hypothetical prote
862	6	2.2	441	2	T22531	hypothetical prote	935	2.2	493	2	A83581	probable c-type cy
863	6	2.2	441	2	C64026	hypothetical prote	936	2.2	493	2	A97439	probable phosphate
864	6	2.2	441	2	E84264	isochorismate synt	937	2.2	493	2	AD2657	phosphate permease
865	6	2.2	441	2	T34032	hypothetical prote	938	2.2	496	2	C83122	probable aldehyde
866	6	2.2	445	2	S73966	MG148 homolog Vxps	939	2.2	496	2	D75293	uracil permease -
867	6	2.2	447	2	S66256	alpha-1,6-mannosyl	940	2.2	497	2	JC4324	aldenhyde dehydrog
868	6	2.2	447	2	C75413	probable proteinas	941	2.2	497	2	B97729	heat shock protein
869	6	2.2	448	2	G95416	probable response	942	2.2	497	2	A96828	hypothetical prote
870	6	2.2	453	2	S52690	hypothetical prote	943	2.2	498	2	H69623	flagellar hook-ass
871	6	2.2	453	2	H64974	hypothetical prote	944	2.2	499	2	D72342	tld protein - The
872	6	2.2	453	2	A98990	hypothetical prote	945	2.2	499	2	S39113	alpha-N-arabinofur
873	6	2.2	453	2	D85835	hypothetical prote	946	2.2	500	1	ITHUC1	complement C1 inh
874	6	2.2	453	2	A50774	hypothetical prote	947	2.2	502	2	T35743	ribosomal protein
875	6	2.2	454	2	C82941	ATP synthase beta	948	2.2	503	2	T29870	hypothetical prote
876	6	2.2	454	2	I64124	virion morphogenes	949	2.2	503	2	S23243	hypothetical prote
877	6	2.2	454	2	H83377	probable transport	950	2.2	504	1	I49428	cytochrome P450 16
878	6	2.2	454	2	S16565	noli protein - Rhi	951	2.2	504	2	T49185	cytokinin oxidase-
879	6	2.2	455	1	S08510	cruciferin precurs	952	2.2	505	2	E83918	carboxypeptidase B
880	6	2.2	455	2	E86169	12S seed storage p	953	2.2	506	2	T28810	hypothetical prote
881	6	2.2	455	2	E83598	signal recognition	954	2.2	506	2	T01716	hypothetical prote
882	6	2.2	456	2	AH0551	proline-specific p	955	2.2	506	2	F85016	probable RING zinc
883	6	2.2	456	2	B86834	sensor protein kin	956	2.2	506	2	B82043	probable sodium/so
884	6	2.2	457	2	B64769	proline transport	957	2.2	507	2	H69186	conserved hypothet
885	6	2.2	457	2	D90685	proline permease t	958	2.2	507	2	T32614	hypothetical prote
886	6	2.2	457	2	H85535	proline permease t	959	2.2	509	2	E90071	zinc metalloprotei
887	6	2.2	457	2	D82961	probable metallopr	960	2.2	510	1	S43692	transcription fact
888	6	2.2	457	2	B82945	chromosomal replic	961	2.2	512	2	B96785	hypothetical prote
889	6	2.2	458	2	S61974	SSU1 protein - yea	962	2.2	513	2	S08381	keratin, 58K type
890	6	2.2	460	2	S35470	NADH2 dehydrogen	963	2.2	514	2	A57280	spindle pole body-
891	6	2.2	461	1	S65187	GPI-anchor biosynt	964	2.2	515	2	E84577	probable cytokinin
892	6	2.2	462	2	B82510	transporter, Nadc	965	2.2	515	2	T40649	hypothetical prote
893	6	2.2	462	2	T27323	hypothetical prote	966	2.2	515	2	PC4419	actin-binding 260K
894	6	2.2	462	2	I51699	gene XGP 5.1C prot	967	2.2	516	2	S34525	hypothetical prote
895	6	2.2	463	2	A10388	probable proline-s	968	2.2	516	2	TQ2389	sucrose transport
896	6	2.2	463	2	S64119	hypothetical prote	969	2.2	516	2	T24729	hypothetical prote
897	6	2.2	464	2	T39699	glutathione-disulf	970	2.2	517	1	A40872	aldenhyde dehydrog
898	6	2.2	464	2	A75615	conserved hypothet	971	2.2	518	2	H97320	PTS system, (possi
899	6	2.2	464	2	AD3639	zinc proteinase (E	972	2.2	518	2	T45765	hypothetical prote
900	6	2.2	465	1	S14762	cruciferin 4 precu	973	2.2	519	2	S60661	legumin - welwisc
901	6	2.2	465	2	F82288	probable proteinas	974	2.2	519	2	T24772	hypothetical prote
902	6	2.2	467	2	A59288	nodulation competi	975	2.2	520	2	T30808	hypothetical prote
903	6	2.2	467	2	T15982	hypothetical prote	976	2.2	522	2	D96913	phosphatase, sulfat
904	6	2.2	468	2	I64182	Na+/H+-exchanging	977	2.2	523	2	T28721	hypothetical prote
905	6	2.2	469	2	AD2909	3-isopropylmalate	978	2.2	524	2	T09937	cytokinin oxidase

979 6 2.2 526 2 T47786  
 980 6 2.2 527 2 D84517  
 981 6 2.2 531 2 E83371  
 982 6 2.2 532 2 F84101  
 983 6 2.2 532 2 B23354  
 984 6 2.2 533 2 S69336  
 985 6 2.2 533 2 T04481  
 986 6 2.2 533 2 S47271  
 987 6 2.2 533 2 A0180  
 988 6 2.2 534 2 T15414  
 989 6 2.2 534 2 T01500  
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 991 6 2.2 535 2 D84340  
 992 6 2.2 536 2 D83622  
 993 6 2.2 537 2 T04944  
 994 6 2.2 538 2 A83632  
 995 6 2.2 538 2 F83622  
 996 6 2.2 541 2 T13496  
 997 6 2.2 541 2 A71649  
 998 6 2.2 543 2 D83262  
 999 6 2.2 543 2 A28671  
 1000 6 2.2 544 2 S62527

ALIGNMENTS

RESULT 1  
 T03734  
 short chain alcohol dehydrogenase homolog - common tobacco  
 N:Alternate names: TFHP-1 protein  
 C:Species: Nicotiana tabacum (common tobacco)  
 C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000  
 C:Accession: T03734  
 R:Kawaoka, A.; Kawamoto, T.; Sekine, M.; Yoshida, K.; Takano, M.; Shimmyo, A.  
 Plant J. 6, 87-97, 1994  
 A>Title: A cis-acting element and a trans-acting factor involved in the wound-induced ex  
 A:Reference number: Z15039; MUID:95004656; PMID:7920706  
 A:Accession: T03734  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <RAW>  
 A:Cross-references: EMBL:D29976; NID:G531268; PIDN:BA06241.1; PID:G531269  
 A:Experimental source: strain cv. Petite Havana SR-1  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 6.2%; Score 17; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 RLEGKVALITGGASGIG 26  
 Db 13 RLEGKVALITGGASGIG 29

RESULT 2  
 T02257  
 probable short chain alcohol dehydrogenase - common tobacco  
 C:Species: Nicotiana tabacum (common tobacco)  
 C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 21-Jul-2000  
 C:Accession: T02257  
 R:Herbers, K.; Moenke, G.; Badur, R.; Sonnenwald, U.  
 Plant Mol. Biol. 29, 1027-1038, 1995  
 A>Title: A simplified procedure for the subtractive cDNA cloning of photoassimilate-resp  
 A:Reference number: S62698; MUID:96145513; PMID:8555446  
 A:Accession: T02257  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-284 <HER>  
 A:Cross-references: EMBL:AJ223177; NID:G2739278; PIDN:CA11153.1; PID:G2739279  
 A:Experimental source: cultivar SNN; tissue-type leaf  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 6.2%; Score 17; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 RLEGKVALITGGASGIG 26  
 Db 13 RLEGKVALITGGASGIG 29

RESULT 3  
 H85039  
 probable alcohol dehydrogenase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Mar-2001  
 C:Accession: H85039  
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999  
 A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: H85039  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-283 <STO>  
 A:Cross-references: GB:NC\_001268; NID:G2720184; PIDN:CAB77799.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: A74G03140  
 A:Map position: 4  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 5.9%; Score 16; DB 2; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 LEGKVALITGGASGIG 26  
 Db 18 LEGKVALITGGASGIG 33

RESULT 4  
 T11579  
 probable short chain alcohol dehydrogenase CPRD12, drought-inducible - cowpea  
 C:Species: Vigna unguiculata (cowpea)  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 20-Jun-2000  
 C:Accession: T11579  
 R:Iuchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.  
 J. Plant Res. 109, 415-424, 1996  
 A>Title: Characterization of two cDNAs for novel drought-inducible genes in the highly d  
 A:Reference number: Z17293  
 A:Accession: T11579  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-267 <IUC>  
 A:Cross-references: EMBL:D88121  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 4.8%; Score 13; DB 2; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 177 AVELGQFGRVNC 189  
 Db 178 AVELGQFGRVNC 190

RESULT 5  
 S39737  
 glucose 1-dehydrogenase homolog ywfd - Bacillus subtilis  
 N:Alternate names: protein ipa-82d  
 N:Contains: probable dehydrogenase (EC 1.1.1.-)  
 C:Species: Bacillus subtilis  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C:Accession: S39737; E70035  
 R:Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,



A.; Rapoport, G.; Danchin, A.  
Mol. Microbiol. 10, 371-384, 1993  
A:Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr  
A:Reference number: S39655; MUID:95020537; PMID:7934828  
A:Accession: S39737  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-255 <GLA>  
A:Cross-references: EMBL:X73124; NID:G413923; PIDN:CAA51638.1; PID:G414006  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993  
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Brn, S.; Brouillet, S.; Pruthi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krog, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrast, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: E70055  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-255 <KUN>  
A:Cross-references: GB:Z99123; GB:AL009126; NID:G2636240; PIDN:CAB15799.1; PID:G2636308  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: wfd  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: NAD; oxidoreductase  
F:8-185/Domain: short-chain alcohol dehydrogenase homology <SADH>  
  
Query Match 3.7%; Score 10; DB 1; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 17 LITGASGIG 26  
|||||  
Db 11 LITGASGIG 20  
  
RESULT 6  
C87434  
2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: C87434  
F:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapito, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: C87434  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <STO>  
A:Cross-references: GB:AE005673; NID:G13422867; PIDN:AAK23471.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CCI492  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
  
Query Match 3.7%; Score 10; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 LEGKVALITG 20  
|||||  
Db 11 LEGKVALITG 20

Db 7 LEGKVALITG 16  
|||||  
RESULT 7  
AD2307  
hypothetical protein alr4011 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AD2307  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AD2307  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-256 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BAW75710.1; PID:G17133146; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr4011  
  
Query Match 3.7%; Score 10; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 17 LITGASGIG 26  
|||||  
Db 24 LITGASGIG 33  
  
RESULT 8  
AB3545  
toluene/sulfonate zinc-independent alcohol dehydrogenase [imported] - Brucella melitensis  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Feb-2002  
C:Accession: AB3545  
R:DeVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AB3545  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-262 <KUR>  
A:Cross-references: GB:AE008918; PIDN:AAL53525.1; PID:G17984431; GSPDB:GN00191  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEII0283  
A:Map position: 11  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
  
Query Match 3.7%; Score 10; DB 2; Length 262;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 LEGKVALITG 20  
|||||  
Db 13 LEGKVALITG 22  
  
RESULT 9  
F96563  
hypothetical protein F19K6.3 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: F96563  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;

ansen, N.P.; Hughes, B.; Huizar, L.  
 Nature 406, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: F96563  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-285 <STO>  
 A:Cross-references: GB:AE005173; NID:g10645436; PIDN:AAAG21552.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F19K6.3  
 A:Map position: 1  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.7%; Score 10; DB 2; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KVALITGGA 22  
 |||||  
 Db 20 KVALITGGA 29  
 |||||

RESULT 10  
 PC4213  
 bphB protein - Comamonas testosteroni (fragment)  
 C:Species: Comamonas testosteroni  
 C:Date: 17-Dec-1996 #sequence\_revision 21-Jan-1997 #text\_change 08-Oct-1999  
 C:Accession: PC4213  
 R:Syvestre, M.; Sirois, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Barria  
 Gene 174, 195-202, 1996  
 A:Title: Sequencing of Comamonas testosteroni strain B-356-biphenyl/chlorobiphenyl dioxy  
 A:Reference number: JC4993; MUID:97045812; PMID:8890734  
 A:Accession: PC4213  
 A:Molecule type: DNA  
 A:Residues: 1-15 <SVL>  
 A:Cross-references: GB:U47637; NID:g1245151; PIDN:AAC44530.1; PID:g1245156  
 A:Experimental source: strain B-356  
 C:Genetics:  
 A:Gene: bphB

Query Match 3.3%; Score 9; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGGAS 23  
 |||||  
 Db 7 VALITGGAS 15  
 |||||

RESULT 11  
 B82680  
 pteridine reductase 1 XFL1457 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: B82680  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A:Reference number: A83515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: B82680  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-245 <SIM>  
 A:Cross-references: GB:AE003975; GB:AE003849; NID:g9106468; PIDN:AAF84266.1; GSPDB:GN001  
 A:Experimental source: strain 9a5c  
 A:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.  
 as-Neto, E.; Docena, C.; El-Dorry, H.; Pacincani, A.P.; Ferreira, A.J.S.  
 submitted to Genbank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohne  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre  
 chado, M.A.; Madaio, A.M.B.N.; Madaio, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
 A:Authors: Martins, E.M.F.; Matsukuma, A.V.; Menck, C.F.M.; Miracca, R.C.; Miyaki, C.Y.;  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 A:Gene: XFL1457  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 0.41;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITGGA 22  
 |||||  
 Db 6 KVALITGGA 14  
 |||||

RESULT 12  
 T02175  
 probable alcohol dehydrogenase At2g47130 [imported] - Arabidopsis thaliana  
 N:Alternate names: hypothetical protein F14M4.4  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
 C:Accession: T02175; D84911  
 R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Rom  
 submitted to the EMBL Data Library, September 1998  
 A:Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.  
 A:Reference number: Z14609  
 A:Accession: T02175  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-257 <ROU>  
 A:Cross-references: EMBL:AC004411; NID:g3522932; PID:g3522935  
 A:Experimental source: cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.  
 euss, D.; Nieman, W.C. White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosomes 2 of the plant *Arabidopsis thaliana*.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: D84911  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-257 <STO>  
 A:Cross-references: GB:AE002093; NID:g3522935; PIDN:AAC34217.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g47130; F14M4.4  
 A:Map position: 2  
 A:Introns: 5/2  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASGIG 26  
 |||||  
 Db 13 ITGGASGIG 21  
 |||||

RESULT 13  
 T02176  
 probable alcohol dehydrogenase At2g47120 [imported] - Arabidopsis thaliana  
 N:Alternate names: hypothetical protein F14M4.5

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
C;Accession: T02176; C84911  
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Rounsley, S.D.; Lin, X.; Kaul, S.; Rounsley, S.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
submitted to the EMBL Data Library, September 1998  
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.  
A;Reference number: Z14609  
A;Accession: T02176  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-258 <ROU>  
A;Cross-references: EMBL:AC004411; NID:G3522932; PID:G3522936  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: C84911  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-258 <STO>  
A;Cross-references: GB:AE002093; NID:G3522936; PIDN:AAC34218.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g47120; F14M4.5  
A;Map position: 2  
A;Introns: 5/2  
A;Note: F14M4.5  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred.No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGASGIG 26  
Db 13 ITGASGIG 21

RESULT 14  
H75616  
oxidoreductase, short-chain dehydrogenase/reductase family - Deinococcus radiodurans (st  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C;Accession: H75616  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: H75616  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-258 <WHI>  
A;Cross-references: GB:AE001862; NID:G6460468; PIDN:AAF12180.1; PID:G646047  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DRA0200  
A;Map position: 2  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred.No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITGG 21  
Db 11 GKVALITGG 19

RESULT 15

AI3149  
3-oxoacyl-(acyl-carrier protein) reductase [imported] - Agrobacterium tumefaciens (strai  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C;Accession: AI3149  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenthrner, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AI3149  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-259 <KUR>  
A;Cross-references: GB:AE008689; PIDN:AAL45615.1; PID:gl7743336; GSPDB:GN00187  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: fabG  
A;Map position: linear chromosome  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 259;  
Best Local Similarity 100.0%; Pred.No. 0.43;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGASGIG 26  
Db 14 ITGASGIG 22

Search completed: October 23, 2003, 13:05:55  
Job time : 85 secs





107	1	214	6	2.2	6	2.2	180	1	282	1	ARDH_YEAST	P50166	candida tro
108	1	216	6	2.2	6	2.2	181	1	283	1	ARDH_YEAST	P3068	saccharomyc
109	1	217	6	2.2	6	2.2	182	1	285	1	YHXC_BACSU	P40397	bacillus su
110	1	218	6	2.2	6	2.2	183	1	286	1	EFTS_XANCP	Q8pmk5	xanthomonas
111	1	219	6	2.2	6	2.2	184	1	292	1	EFTS_XANCP	Q8pmk5	xanthomonas
112	1	220	6	2.2	6	2.2	185	1	297	1	OXIR_STRLI	P53120	streptomyce
113	1	221	6	2.2	6	2.2	186	1	298	1	OXIR_STRLI	Q03326	streptomyce
114	1	222	6	2.2	6	2.2	187	1	300	1	ERA_MYCTU	O05834	mycobacteri
115	1	223	6	2.2	6	2.2	188	1	301	1	YJHH_ECOLI	P93359	escherichia
116	1	224	6	2.2	6	2.2	189	1	310	1	YJHH_ECOLI	P93359	escherichia
117	1	225	6	2.2	6	2.2	190	1	311	1	YJHH_ECOLI	P93359	escherichia
118	1	226	6	2.2	6	2.2	191	1	312	1	YJHH_ECOLI	P93359	escherichia
119	1	227	6	2.2	6	2.2	192	1	313	1	YJHH_ECOLI	P93359	escherichia
120	1	228	6	2.2	6	2.2	193	1	314	1	YJHH_ECOLI	P93359	escherichia
121	1	229	6	2.2	6	2.2	194	1	315	1	YJHH_ECOLI	P93359	escherichia
122	1	230	6	2.2	6	2.2	195	1	316	1	YJHH_ECOLI	P93359	escherichia
123	1	231	6	2.2	6	2.2	196	1	317	1	YJHH_ECOLI	P93359	escherichia
124	1	232	6	2.2	6	2.2	197	1	318	1	YJHH_ECOLI	P93359	escherichia
125	1	233	6	2.2	6	2.2	198	1	319	1	YJHH_ECOLI	P93359	escherichia
126	1	234	6	2.2	6	2.2	199	1	320	1	YJHH_ECOLI	P93359	escherichia
127	1	235	6	2.2	6	2.2	200	1	321	1	YJHH_ECOLI	P93359	escherichia
128	1	236	6	2.2	6	2.2	201	1	322	1	YJHH_ECOLI	P93359	escherichia
129	1	237	6	2.2	6	2.2	202	1	323	1	YJHH_ECOLI	P93359	escherichia
130	1	238	6	2.2	6	2.2	203	1	324	1	YJHH_ECOLI	P93359	escherichia
131	1	239	6	2.2	6	2.2	204	1	325	1	YJHH_ECOLI	P93359	escherichia
132	1	240	6	2.2	6	2.2	205	1	326	1	YJHH_ECOLI	P93359	escherichia
133	1	241	6	2.2	6	2.2	206	1	327	1	YJHH_ECOLI	P93359	escherichia
134	1	242	6	2.2	6	2.2	207	1	328	1	YJHH_ECOLI	P93359	escherichia
135	1	243	6	2.2	6	2.2	208	1	329	1	YJHH_ECOLI	P93359	escherichia
136	1	244	6	2.2	6	2.2	209	1	330	1	YJHH_ECOLI	P93359	escherichia
137	1	245	6	2.2	6	2.2	210	1	331	1	YJHH_ECOLI	P93359	escherichia
138	1	246	6	2.2	6	2.2	211	1	332	1	YJHH_ECOLI	P93359	escherichia
139	1	247	6	2.2	6	2.2	212	1	333	1	YJHH_ECOLI	P93359	escherichia
140	1	248	6	2.2	6	2.2	213	1	334	1	YJHH_ECOLI	P93359	escherichia
141	1	249	6	2.2	6	2.2	214	1	335	1	YJHH_ECOLI	P93359	escherichia
142	1	250	6	2.2	6	2.2	215	1	336	1	YJHH_ECOLI	P93359	escherichia
143	1	251	6	2.2	6	2.2	216	1	337	1	YJHH_ECOLI	P93359	escherichia
144	1	252	6	2.2	6	2.2	217	1	338	1	YJHH_ECOLI	P93359	escherichia
145	1	253	6	2.2	6	2.2	218	1	339	1	YJHH_ECOLI	P93359	escherichia
146	1	254	6	2.2	6	2.2	219	1	340	1	YJHH_ECOLI	P93359	escherichia
147	1	255	6	2.2	6	2.2	220	1	341	1	YJHH_ECOLI	P93359	escherichia
148	1	256	6	2.2	6	2.2	221	1	342	1	YJHH_ECOLI	P93359	escherichia
149	1	257	6	2.2	6	2.2	222	1	343	1	YJHH_ECOLI	P93359	escherichia
150	1	258	6	2.2	6	2.2	223	1	344	1	YJHH_ECOLI	P93359	escherichia
151	1	259	6	2.2	6	2.2	224	1	345	1	YJHH_ECOLI	P93359	escherichia
152	1	260	6	2.2	6	2.2	225	1	346	1	YJHH_ECOLI	P93359	escherichia
153	1	261	6	2.2	6	2.2	226	1	347	1	YJHH_ECOLI	P93359	escherichia
154	1	262	6	2.2	6	2.2	227	1	348	1	YJHH_ECOLI	P93359	escherichia
155	1	263	6	2.2	6	2.2	228	1	349	1	YJHH_ECOLI	P93359	escherichia
156	1	264	6	2.2	6	2.2	229	1	350	1	YJHH_ECOLI	P93359	escherichia
157	1	265	6	2.2	6	2.2	230	1	351	1	YJHH_ECOLI	P93359	escherichia
158	1	266	6	2.2	6	2.2	231	1	352	1	YJHH_ECOLI	P93359	escherichia
159	1	267	6	2.2	6	2.2	232	1	353	1	YJHH_ECOLI	P93359	escherichia
160	1	268	6	2.2	6	2.2	233	1	354	1	YJHH_ECOLI	P93359	escherichia
161	1	269	6	2.2	6	2.2	234	1	355	1	YJHH_ECOLI	P93359	escherichia
162	1	270	6	2.2	6	2.2	235	1	356	1	YJHH_ECOLI	P93359	escherichia
163	1	271	6	2.2	6	2.2	236	1	357	1	YJHH_ECOLI	P93359	escherichia
164	1	272	6	2.2	6	2.2	237	1	358	1	YJHH_ECOLI	P93359	escherichia
165	1	273	6	2.2	6	2.2	238	1	359	1	YJHH_ECOLI	P93359	escherichia
166	1	274	6	2.2	6	2.2	239	1	360	1	YJHH_ECOLI	P93359	escherichia
167	1	275	6	2.2	6	2.2	240	1	361	1	YJHH_ECOLI	P93359	escherichia
168	1	276	6	2.2	6	2.2	241	1	362	1	YJHH_ECOLI	P93359	escherichia
169	1	277	6	2.2	6	2.2	242	1	363	1	YJHH_ECOLI	P93359	escherichia
170	1	278	6	2.2	6	2.2	243	1	364	1	YJHH_ECOLI	P93359	escherichia
171	1	279	6	2.2	6	2.2	244	1	365	1	YJHH_ECOLI	P93359	escherichia
172	1	280	6	2.2	6	2.2	245	1	366	1	YJHH_ECOLI	P93359	escherichia
173	1	281	6	2.2	6	2.2	246	1	367	1	YJHH_ECOLI	P93359	escherichia
174	1	282	6	2.2	6	2.2	247	1	368	1	YJHH_ECOLI	P93359	escherichia
175	1	283	6	2.2	6	2.2	248	1	369	1	YJHH_ECOLI	P93359	escherichia
176	1	284	6	2.2	6	2.2	249	1	370	1	YJHH_ECOLI	P93359	escherichia
177	1	285	6	2.2	6	2.2	250	1	371	1	YJHH_ECOLI	P93359	escherichia
178	1	286	6	2.2	6	2.2	251	1	372	1	YJHH_ECOLI	P93359	escherichia
179	1	287	6	2.2	6	2.2	252	1	373	1	YJHH_ECOLI	P93359	escherichia

253 P50525 schizosacch 366 1 APN1\_SCHPO  
 254 P12441 influenza b 366 1 HEMA\_INBID  
 255 P55431 rhizobium s 366 1 NOLL\_RHISN  
 256 P53778 homo sapien 367 1 MK12\_HUMAN  
 257 P81294 juniperus a 367 1 MPAL\_JUNAS  
 258 P9KXRT streptomyce 368 1 PYRD\_STRCO  
 259 Q53915 streptomyce 368 1 RF2\_STRCO  
 260 Q53558 rhodobacter 369 1 CHEB\_RHOSH  
 261 Q8NQA1 corynebacte 370 1 HEMZ\_CORGL  
 262 Q9P0M6 homo sapien 371 1 H2AW\_HUMAN  
 263 Q8O547 homo sapien 372 1 GNDS\_HUMAN  
 264 P86332 cryptospori 374 1 SBP\_CRYPA  
 265 P26183 cryptospori 376 1 ACT\_CRYPV  
 266 Q8FTC6 corynebacte 377 1 PYRD\_COREF  
 267 P38127 streptomyce 377 1 RIM2\_YEAST  
 268 P46080 anabaena sp 378 1 VN91\_ANASP  
 269 P19333 torpedo cal 379 1 VAT1\_TORCA  
 270 P07789 bacillus su 380 1 COTB\_EACSU  
 271 P31005 bacillus me 380 1 MEDH\_BACWT  
 272 P49833 odontella s 380 1 YCX7\_ODOSI  
 273 P73532 synechocyst 381 1 RECF\_SYNY3  
 274 Q01459 homo sapien 385 1 DIAC\_HUMAN  
 275 Q9U5N1 manduca sex 385 1 VATC\_MANSE  
 276 Q9Y020 ralsstontia s 386 1 HISZ\_RALSO  
 277 P15587 streptomyce 386 1 XYL4\_STROL  
 278 Q20252 spinacia ol 387 1 S17P\_SPIOL  
 279 Q27181 paramacium 387 1 T2C\_PARTE  
 280 Q910B8 streptomyce 387 1 XYL4\_STRCO  
 281 P24300 streptomyce 387 1 XYL4\_STRKU  
 282 P04165 zea mays (m 388 1 CYB\_MAIZE  
 283 P50910 streptomyce 388 1 XYL4\_STRDI  
 284 Q91558 streptomyce 388 1 XYL4\_STRTM  
 285 P24299 streptomyce 390 1 XYL4\_STRAL  
 286 Q9ZZT8 pisum sativ 392 1 CYB\_BEA  
 287 P29757 solanum tub 392 1 CYB\_SOLTU  
 288 P05718 vicia faba 392 1 CYB\_VICFA  
 289 P42792 arabidopsis 393 1 CYB\_ARATH  
 290 P37030 bradyrhizob 393 1 NIFS\_BRAJA  
 291 P09843 oenothera b 394 1 CYB\_DENBE  
 292 Q19913 cyanidium c 396 1 YC44\_CYACA  
 293 P14833 oryza sativ 397 1 CYB\_ORYSA  
 294 Q94837 daucus caro 398 1 CYB\_DAUCA  
 295 P07747 triticum ae 398 1 CYB\_WHEAT  
 296 P17560 sus scrofa 402 1 RNBP\_PIG  
 297 Q09780 schizosacch 404 1 KIME\_SCHPO  
 298 Q58860 methanococc 405 1 THRC\_METJA  
 299 P77444 escherichia 406 1 CSDB\_ECOLI  
 300 P47693 mycoplasma 407 1 SYI\_MYCGE  
 301 Q53598 streptococc 413 1 NEUA\_STR3A  
 302 Q9AF99 streptococc 413 1 NEUA\_STR5A  
 303 Q9HIM0 thermoplas 414 1 PYRC\_THEAC  
 304 P17630 sus scrofa 416 1 HAPC\_PIG  
 305 P51606 homo sapien 417 1 RNBP\_HUMAN  
 306 P49424 pseudomonas 419 1 MANA\_PSEFL  
 307 P13266 escherichia 419 1 NEUA\_ECOLI  
 308 P82343 mus musculu 419 1 RNBP\_MOUSE  
 309 P51607 rattus norv 419 1 RNBP\_RAT  
 310 Q9RUV5 deinococcus 425 1 SYS\_DEIRA  
 311 Q970N1 sulfolobus 431 1 TRB2\_SULTO  
 312 TC01\_HUMAN 433 1 TC01\_HUMAN  
 313 Q9RPF2 pseudomonas 438 1 MNT2\_PSEAE  
 314 XYL4\_RUMFL 438 1 XYL4\_RUMFL  
 315 RNR\_THIFE 439 1 RNR\_THIFE  
 316 YD40\_HAEIN 441 1 YD40\_HAEIN  
 317 VATC\_DROME 442 1 VATC\_DROME  
 318 QPSP\_PETMA 444 1 OPSP\_PETMA  
 319 Q83325 bacillus me 445 1 Y148\_MYCPN  
 320 P75584 mycoplasma 445 1 Y148\_MYCPN  
 321 GNT2\_HUMAN 447 1 GNT2\_HUMAN  
 322 YEGQ\_ECOLI 453 1 YEGQ\_ECOLI  
 323 P45217 haemophilus 454 1 YB62\_HAEIN  
 324 P15456 arabidopsis 455 1 12S2\_ARATH  
 325 P37460 salmonella 456 1 PROV\_SALTY

326 6 2.2 457 1 ARLY\_PASMU  
 327 6 2.2 457 1 DNAA\_UREPA  
 328 6 2.2 457 1 PROV\_ECOLI  
 329 6 2.2 458 1 SSU1\_YEAST  
 330 6 2.2 460 1 NU4M\_CROLA  
 331 6 2.2 461 1 GP13\_YEAST  
 332 6 2.2 461 1 Y514\_HUMAN  
 333 6 2.2 463 1 COAT\_FRG3V  
 334 6 2.2 463 1 COAT\_RTRV  
 335 6 2.2 463 1 SIL9\_HUMAN  
 336 6 2.2 463 1 YGL1\_YEAST  
 337 6 2.2 464 1 CAPB\_EACAN  
 338 6 2.2 464 1 GSHR\_SCHPO  
 339 6 2.2 465 1 CRU4\_BRANA  
 340 6 2.2 465 1 MPPB\_BLAEM  
 341 6 2.2 467 1 SIL7\_HUMAN  
 342 6 2.2 468 1 DCMG\_METTE  
 343 6 2.2 468 1 YB07\_HAEIN  
 344 6 2.2 469 1 LEU2\_AGRIS  
 345 6 2.2 469 1 LEU2\_RHIL0  
 346 6 2.2 469 1 LEU2\_RHIME  
 347 6 2.2 470 1 SELA\_MOOTH  
 348 6 2.2 472 1 PEDA\_STRPY  
 349 6 2.2 473 1 T115\_CLOPE  
 350 6 2.2 474 1 DLDH\_ALCEU  
 351 6 2.2 476 1 CBPH\_HUMAN  
 352 6 2.2 476 1 CBPH\_MOUSE  
 353 6 2.2 476 1 CBPH\_RAT  
 354 6 2.2 477 1 DLDH\_PSEFL  
 355 6 2.2 477 1 TRPC\_HAEIN  
 356 6 2.2 479 1 6PGD\_TRYBB  
 357 6 2.2 481 1 LMRA\_STRLN  
 358 6 2.2 483 1 KPYK\_METEX  
 359 6 2.2 484 1 PANP\_HAEIN  
 360 6 2.2 485 1 SAHH\_PETCR  
 361 6 2.2 487 1 YOW5\_CABEL  
 362 6 2.2 488 1 GATA\_AERPE  
 363 6 2.2 492 1 YD48\_SCHPO  
 364 6 2.2 496 1 GSHR\_ORYSA  
 365 6 2.2 497 1 DHAL\_ENCBU  
 366 6 2.2 497 1 FXD2\_HUMAN  
 367 6 2.2 498 1 FLID\_BACSU  
 368 6 2.2 499 1 ABFB\_ASPNG  
 369 6 2.2 500 1 IC1\_HUMAN  
 370 6 2.2 501 1 CKX2\_ARATH  
 371 6 2.2 502 1 MYOC\_RAT  
 372 6 2.2 509 1 AURE\_STAAU  
 373 6 2.2 510 1 ERM\_HUMAN  
 374 6 2.2 512 1 K2C5\_XENLA  
 375 6 2.2 514 1 SAD1\_SCHPO  
 376 6 2.2 516 1 YC82\_EUGGR  
 377 6 2.2 517 1 DHAS\_HUMAN  
 378 6 2.2 520 1 AMPA\_MYCSA  
 379 6 2.2 521 1 VL2\_HPV04  
 380 6 2.2 523 1 CKX3\_ARATH  
 381 6 2.2 524 1 CKX4\_ARATH  
 382 6 2.2 532 1 FLID\_BACHD  
 383 6 2.2 533 1 MLO\_HORVU  
 384 6 2.2 534 1 AMT1\_CABEL  
 385 6 2.2 534 1 CKX1\_MAIZE  
 386 6 2.2 535 1 ARS\_PSEAE  
 387 6 2.2 541 1 AAAT\_RABIT  
 388 6 2.2 541 1 ACEA\_YARLI  
 389 6 2.2 541 1 MLES\_OENOE  
 390 6 2.2 543 1 DAL5\_YEAST  
 391 6 2.2 544 1 YC9D\_SCHPO  
 392 6 2.2 546 1 PHR2\_CANAL  
 393 6 2.2 546 1 PYRG\_VIBPA  
 394 6 2.2 547 1 ILVD\_ARCFU  
 395 6 2.2 548 1 PPAC\_THEMEA  
 396 6 2.2 552 1 K2C6\_MOUSE  
 397 6 2.2 555 1 ILVD\_AQUAE  
 398 6 2.2 555 1 ILVD\_BACHD

P57909 pasteurella  
 Q9PR22 ureaplasma  
 P77327 escherichia  
 P41930 saccharomyc  
 P34194 crossostoma  
 P32363 saccharomyc  
 Q60269 homo sapien  
 Q67473 frog virus  
 Q9Y1Q8 rana tigrin  
 Q9Y336 homo sapien  
 P53116 saccharomyc  
 P19580 bacillus an  
 P78965 schizosacch  
 P33522 brassica na  
 Q00302 blastoclad  
 Q9Y286 homo sapien  
 Q50539 methanosarc  
 Q57007 haemophilus  
 Q8UBY9 agrobacteri  
 Q98EFI rhizobium l  
 Q92176 rhizobium m  
 Q32277 morella th  
 Q9A0M0 streptococc  
 Q53309 clostridium  
 P52992 alcaligenes  
 P16870 homo sapien  
 Q00493 mus musculu  
 P15087 rattus norv  
 P14218 pseudomonas  
 P46451 haemophilus  
 P31072 trypanosoma  
 P46104 streptomyce  
 Q05118 methylobact  
 P44963 haemophilus  
 Q01781 petrobelinu  
 P30651 caenorhabdi  
 Q9YB80 aeropyrum p  
 Q10301 schizosacch  
 P48642 oryza sativ  
 Q27640 enchytraeus  
 Q60548 homo sapien  
 P39738 bacillus su  
 P42255 aspergillus  
 P05155 homo sapien  
 Q9FUI3 arabidopsis  
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 Q9K6M0 bacillus ha  
 P33766 hordeum vul  
 P47707 mycoplasma  
 Q07862 human papil  
 P54145 caenorhabdi  
 P490N8 zea mays (m  
 P51691 pseudomonas  
 P19105 oryctolagus  
 Q48756 oenococcus  
 P15365 saccharomyc  
 Q09887 schizosacch  
 O13318 candida alb  
 Q871P9 vibrio para  
 Q29248 archaeoglob  
 Q9WZ56 thermotoga  
 K2C6\_MOUSE  
 Q67009 aquifex aeo  
 Q9K8E4 bacillus ha

399	6	2.2	556	1	RS1_HELPY	P56008	helicobacte	472	6	2.2	725	1	RNR_MYCPE	P47350	mycoplasma
400	6	2.2	556	1	SYDC_YEAST	P04802	saccharomyc	473	6	2.2	726	1	RNR_MYCPN	P75529	mycoplasma
401	6	2.2	557	1	CAR1_AQUAE	O67869	aquifex_ao	474	6	2.2	728	1	GSH1_NEUCR	O8x0x0	neurospora
402	6	2.2	557	1	ILVD_AERPE	O9v988	aeropyrum_p	475	6	2.2	730	1	DCOR_LACS3	P43099	lactobacilli
403	6	2.2	557	1	ILVD_BACSU	Y11985	bacillus_su	476	6	2.2	730	1	FOG_DROVE	P40795	drosophila
404	6	2.2	557	1	Y369_MYCGB	P47609	mycoplasma	477	6	2.2	731	1	RNR_BUCAL	P57628	buchnera_ap
405	6	2.2	560	1	ILVD_SULTO	Q96yK0	sulfolobus	478	6	2.2	733	1	SUF_DROME	P25991	drosophila
406	6	2.2	560	1	KG59_YEAST	P43637	saccharomyc	479	6	2.2	736	1	PRX1_CHICK	O91018	gallus_gall
407	6	2.2	567	1	COX1_EMENI	P00402	emeritella	480	6	2.2	736	1	PRX1_HUMAN	Q92786	homo sapien
408	6	2.2	574	1	HENA_INBND	P10461	influenza_b	481	6	2.2	737	1	PRX1_MOUSE	P48437	mus musculus
409	6	2.2	575	1	HENA_INBEO	P10448	influenza_b	482	6	2.2	751	1	PA26_RAT	P97570	rattus norv
410	6	2.2	575	1	HENA_INBHK	P10448	influenza_b	483	6	2.2	752	1	PA26_MOUSE	P97819	mus musculus
411	6	2.2	576	1	DEAI_ANASP	Q8ytw5	anaeana_sp	484	6	2.2	768	1	PURL_SINY3	P72644	synecocyst
412	6	2.2	576	1	HENA_INBNS	P09765	influenza_b	485	6	2.2	769	1	COMP_BACSU	O99037	bacillus_su
413	6	2.2	578	1	HENA_INBNE	P09765	influenza_b	486	6	2.2	781	1	IORB_BREDI	O51698	brevundimon
414	6	2.2	578	1	HENA_INBVI	P09767	influenza_b	487	6	2.2	782	1	RNR_HAEIN	P44907	haemophilus
415	6	2.2	578	1	VATA_METAC	O8t1j1	methanosarc	488	6	2.2	797	1	AF32_HUMAN	Q9y4w6	homo sapien
416	6	2.2	578	1	VATA_METWA	O60186	methanosarc	489	6	2.2	803	1	SYFB_WIGER	Q8d3b5	wiggleswort
417	6	2.2	579	1	SYN3_RAT	O70441	rattus norv	490	6	2.2	804	1	YNA4_CABEL	P45895	caenorhabdi
418	6	2.2	583	1	HENA_INBEN	P10757	influenza_b	491	6	2.2	806	1	PA26_HUMAN	O60733	homo sapien
419	6	2.2	583	1	HENA_INBOR	P03464	influenza_b	492	6	2.2	813	1	RNR_ECOLI	P21499	escherichia
420	6	2.2	583	1	HENA_INBSI	P03464	influenza_b	493	6	2.2	813	1	RNR_SHIFL	P30851	shigella_fl
421	6	2.2	584	1	HENA_INBLE	P03460	influenza_b	494	6	2.2	814	1	P3K1_SOYBN	P42347	glycine_max
422	6	2.2	585	1	HENA_INBRE	P17504	influenza_b	495	6	2.2	817	1	PG40_HUMAN	O75420	homo sapien
423	6	2.2	585	1	HENA_INBVK	P22092	influenza_b	496	6	2.2	817	1	YG4B_YEAST	P46951	saccharomyc
424	6	2.2	585	1	VATA_THERH	P56403	thermus_ther	497	6	2.2	821	1	RNR_VIBCH	O9kny1	vibrio_chol
425	6	2.2	593	1	COX1_HALNI	P33518	halobacteri	498	6	2.2	824	1	TCG3_MOUSE	O61371	mus musculus
426	6	2.2	593	1	SILL_HUMAN	Q96pQ1	homo sapien	499	6	2.2	825	1	S85_RAT	P25002	halobacteri
427	6	2.2	597	1	SILL_PANTR	Q951n0	pan troglod	500	6	2.2	827	1	CSG_HALVO	P40611	vibrio para
428	6	2.2	605	1	BRU1_BEV	P03209	epstein-bar	501	6	2.2	835	1	TOPI_VIBPA	P34185	synecococc
429	6	2.2	607	1	AB2_XENLA	P14872	xenopus lae	502	6	2.2	839	1	TOPI_SINYL	P81073	phycomoc
430	6	2.2	607	1	HRA1_XANCV	F80151	xanthomonas	503	6	2.2	841	1	CHS1_PHEB7	P49917	homo sapien
431	6	2.2	607	1	PEPF_MYCGB	P47429	mycoplasma	504	6	2.2	844	1	DNL4_HUMAN	P43244	rattus norv
432	6	2.2	609	1	FEPA_HORSE	P49066	equus cabal	505	6	2.2	845	1	MAT3_RAT	P43244	rattus norv
433	6	2.2	611	1	GIDA_MYCPU	Q98qv8	mycoplasma	506	6	2.2	847	1	MAT3_HUMAN	P43244	homo sapien
434	6	2.2	611	1	PEPF_MYCPN	P54125	mycoplasma	507	6	2.2	848	1	CLPB_MYCTU	O53719	mycobacteri
435	6	2.2	614	1	GLMS_STROO	O86781	s_glucoam	508	6	2.2	853	1	CNRB_BOVIN	P23439	bos taurus
436	6	2.2	614	1	YDNK_LACLC	P42377	lactococcus	509	6	2.2	853	1	TOP1_BUCAP	Q9k9p7	buchnera_ap
437	6	2.2	618	1	CAB2_HLVTA	Q58776	methanococc	510	6	2.2	854	1	CNRB_HUMAN	P35913	homo sapien
438	6	2.2	619	1	BCHD_CHLVI	O50313	chlorobium	511	6	2.2	856	1	CLPB_HAEIN	P44403	haemophilus
439	6	2.2	620	1	RECH_CHLTE	O04864	homo sapien	512	6	2.2	861	1	MVP_MOUSE	Q9eqk5	mus musculus
440	6	2.2	620	1	BCHD_CHLTE	Q93sw0	chlorobium	513	6	2.2	866	1	POG3_ARATH	Q9t052	arabidopsis
441	6	2.2	621	1	ASPA_AERSA	P11339	aeromonas_s	514	6	2.2	866	1	RECE_ECOLI	Q9t052	escherichia
442	6	2.2	621	1	SRPR_YEAST	P12916	saccharomyc	515	6	2.2	871	1	UL47_HSVBE	P28929	equine herp
443	6	2.2	623	1	GLMS_MYCTU	O06253	m_glucoam	516	6	2.2	872	1	CLPB_SINY3	P74361	synecocyst
444	6	2.2	624	1	GLMS_MYCLE	P40831	m_glucoam	517	6	2.2	884	1	SYA_RALSO	O8y193	raistronia_s
445	6	2.2	625	1	SVR_SULSO	Q972x1	sulfolobus	518	6	2.2	887	1	SYA_AGRTS	O8y193	raistronia_s
446	6	2.2	627	1	GLMS_MYCSM	O68956	m_glucoam	519	6	2.2	889	1	ISRB_CHICK	O8ue87	agrobacteri
447	6	2.2	633	1	SNF1_YEAST	P06782	saccharomyc	520	6	2.2	892	1	RA16_SCHPO	P36617	schizosacch
448	6	2.2	636	1	FTHS_SPTOL	P28723	spinacia_ol	521	6	2.2	893	1	WPC_HUMAN	Q14764	homo sapien
449	6	2.2	636	1	UVBI_NEUCR	Q01408	neurospora	522	6	2.2	898	1	ACOC_CUGWA	P49608	cucurbita_m
450	6	2.2	659	1	SPA2_SINY3	P72587	synecocyst	523	6	2.2	899	1	VI20_HSVSA	Q01055	herpesvirus
451	6	2.2	662	1	VGLF_CDVO	P12569	canine dist	524	6	2.2	901	1	SOK1_YEAST	P40317	saccharomyc
452	6	2.2	663	1	AF31_MOUSE	Q920a7	mus musculus	525	6	2.2	902	1	ITH1_PIG	Q99052	sus scrofa
453	6	2.2	663	1	OTRA_STREM	Q95002	streptomyce	526	6	2.2	907	1	ITH1_MOUSE	Q61702	mus musculus
454	6	2.2	663	1	Y4WM_RHISN	P55691	rhizobium_s	527	6	2.2	907	1	LGR5_HUMAN	O75473	homo sapien
455	6	2.2	666	1	VO01_VARV	P34010	variola vir	528	6	2.2	911	1	CTNA_DRONE	P19827	homo sapien
456	6	2.2	668	1	DNLJ_BACSU	Q31498	bacillus_su	529	6	2.2	917	1	CC15_SCHPO	P35220	drosophila
457	6	2.2	669	1	EFGL_SINY3	Q55421	synecocyst	530	6	2.2	927	1	DNL1_CANAL	Q09822	schizosacch
458	6	2.2	671	1	PTGA_CORGL	Q45298	corynebacte	531	6	2.2	928	1	DPOM_MAIZE	P52496	candida alb
459	6	2.2	677	1	FXP1_HUMAN	Q9h334	homo sapien	532	6	2.2	929	1	CITC_HUMAN	P10582	zea mays (m
460	6	2.2	683	1	PTNA_CORGL	O46072	corynebacte	533	6	2.2	934	1	CITC_RAT	P11586	h c-1-tetra
461	6	2.2	687	1	FSHR_SQUAS	Q95179	equus asinu	534	6	2.2	938	1	LEVR_BACSU	P27653	r c-1-tetra
462	6	2.2	693	1	HAA1_HUMAN	P49915	homo sapien	535	6	2.2	944	1	IF2_HELPY	P23914	bacillus_su
463	6	2.2	694	1	HAA1_YEAST	Q12753	saccharomyc	536	6	2.2	949	1	IF2_HELPJ	P59772	helicobacte
464	6	2.2	697	1	SRSP_CABEL	P41848	caenorhabdi	537	6	2.2	960	1	OPAI_HUMAN	Q92m46	helicobacte
465	6	2.2	697	1	E75_MANSE	Q08893	manduca sex	538	6	2.2	960	1	OPAI_MOUSE	O60313	homo sapien
466	6	2.2	705	1	FXP1_MOUSE	P58462	mus musculus	539	6	2.2	960	1	OPAI_MOUSE	P58281	mus musculus
467	6	2.2	709	1	NUSC_PACAC	Q9mVX2	pachira aqu	540	6	2.2	972	1	CSF1_ARATH	Q92P77	arabidopsis
468	6	2.2	714	1	CLPB_MYCGB	P47537	mycoplasma	541	6	2.2	974	1	FOD1_CAUCR	Q92P78	caulobacter
469	6	2.2	718	1	ATKB_AGRTS	Q9u9d9	agrobacteri	542	6	2.2	976	1	FIBP_ADER3	Q93353	bovine aden
470	6	2.2	718	1	PLSB_CAREL	Q22949	caenorhabdi	543	6	2.2	994	1	ATAI_CHICK	P13585	g sarcopias
471	6	2.2	721	1	THIC_SHEON	Q9eed7	shewanella	544	6	2.2	994	1	ATAI_PANES	Q92105	r sarcopias



545	6	2.2	997	1	ATA2_CANPA	O46674	c sarcoplas	618	6	2.2	1938	1	MYSD_CABEL	P02567	caenorhabdi
546	6	2.2	997	1	ATA2_FELCA	Q00779	f sarcoplas	619	6	2.2	1947	1	MYSC_CABEL	P12845	caenorhabdi
547	6	2.2	998	1	RRPO_BBV	Q06631	black beetl	620	6	2.2	1962	1	MYSA_DROME	P05661	drosophila
548	6	2.2	998	1	RRPO_FHV	Q66929	flock house	621	6	2.2	1966	1	MYSB_CABEL	P02566	caenorhabdi
549	6	2.2	999	1	ATA3_RAT	P18596	rattus norv	622	6	2.2	1969	1	MYSA_CABEL	P12844	caenorhabdi
550	6	2.2	999	1	MPD_HELPY	Q26066	helicobacte	623	6	2.2	2130	1	BA2B_CHICK	Q9dell3	gallus gall
551	6	2.2	1007	1	CHC2_HUMAN	Q9514	homo sapien	624	6	2.2	2210	1	RRPL_EBOSM	Q66802	ebola virus
552	6	2.2	1014	1	ODO1_YEAST	P20967	saccharomyc	625	6	2.2	2514	1	POLN_ONNVG	P13886	o'nyong-nyo
553	6	2.2	1027	1	CARY_BACSU	P18185	bacillus su	626	6	2.2	2542	1	TLN2_HUMAN	Q9y496	homo sapien
554	6	2.2	1033	1	YD56_SCHPO	O10309	schizosacch	627	6	2.2	2647	1	FLNA_HUMAN	P21333	homo sapien
555	6	2.2	1035	1	DROL_RHGM6	O71121	rhesus cyto	628	6	2.2	2713	1	CHD5_HUMAN	Q8td26	homo sapien
556	6	2.2	1038	1	ATA3_MOUSE	Q64518	mus musculus	629	6	2.2	2960	1	AHMK_HUMAN	Q09666	homo sapien
557	6	2.2	1040	1	YEGN_ECOLI	P76398	escherichia	630	6	2.2	3388	1	POLG_DEN2P	P12823	d genome po
558	6	2.2	1041	1	ATA2_CHICK	Q03669	g sarcoplas	631	6	2.2	3391	1	POLG_DEN26	P29990	d genome po
559	6	2.2	1041	1	EGT2_YEAST	P42835	saccharomyc	632	6	2.2	3391	1	POLG_DEN27	P29991	d genome po
560	6	2.2	1042	1	ATA2_HUMAN	P16615	h sarcoplas	633	6	2.2	3391	1	POLG_DEN2J	P07564	d genome po
561	6	2.2	1042	1	ATA2_PIG	P11607	s sarcoplas	634	6	2.2	3391	1	POLG_DEN2N	P14340	d genome po
562	6	2.2	1042	1	ATA2_RABIT	P20647	o sarcoplas	635	6	2.2	3801	1	LYST_HUMAN	Q9y698	homo sapien
563	6	2.2	1042	1	ATA3_CHICK	Q9ygl9	gallus gall	636	6	2.2	4036	1	RRPL_DUGBV	Q66431	dugbe virus
564	6	2.2	1043	1	ATA2_RAT	P11507	r sarcoplas	637	6	2.2	4349	1	FAT2_HUMAN	Q9nyq8	homo sapien
565	6	2.2	1044	1	ATA2_MOUSE	O55143	m sarcoplas	638	6	2.2	4427	1	PKSL_BACSU	Q05470	bacillus su
566	6	2.2	1054	1	CYPE_BACSU	O08336	bacillus su	639	6	2.2	4447	1	PKSK_BACSU	P40803	bacillus su
567	6	2.2	1064	1	CARB_BACST	O50302	bacillus st	640	6	2.2	4563	1	APB_HUMAN	P04114	homo sapien
568	6	2.2	1065	1	CARB_BACCL	P46537	bacillus ca	641	6	2.2	5938	1	MAC4_HUMAN	Q96pk2	homo sapien
569	6	2.2	1065	1	NOLG_RHIME	P25197	rhizobium m	642	5	1.8	15	1	DIDH_PSESP	P80701	pseudomonas
570	6	2.2	1066	1	HYSA_STRPN	Q54873	stretococc	643	5	1.8	18	1	YMDB_CHIUA	Q45827	chloroflexu
571	6	2.2	1067	1	CARB_CLOPE	O84hb3	clostridium	644	5	1.8	33	1	ALOX_PICPA	P04842	ichia past
572	6	2.2	1071	1	CARB_BACSU	P25994	bacillus su	645	5	1.8	42	1	YPI_BPPED	P27386	bacterioph
573	6	2.2	1072	1	SYIC_YEAST	P09436	saccharomyc	646	5	1.8	46	1	LHA1_ECTHA	P80100	ectothiorho
574	6	2.2	1074	1	PLD1_HUMAN	Q13393	homo sapien	647	5	1.8	47	1	LHA2_ECTHA	P80101	ectothiorho
575	6	2.2	1076	1	CARB_BUCBP	P59448	buchnera ap	648	5	1.8	47	1	Y311_TREPA	O83333	treponema p
576	6	2.2	1076	1	IF3A_CABEL	P34339	caenorhabdi	649	5	1.8	49	1	RPOP_PYRAB	Q9v201	pyrococcus
577	6	2.2	1076	1	NUPI_YEAST	P20676	saccharomyc	650	5	1.8	49	1	RPOP_PYRFU	O8tzi3	pyrococcus
578	6	2.2	1088	1	KGP2_DROME	Q30443	drosophila	651	5	1.8	49	1	RPOP_PYRHO	O74105	pyrococcus
579	6	2.2	1099	1	CARB_THENA	Q9wz27	thermotoga	652	5	1.8	54	1	AMAI_ALIMI	P40641	alligator m
580	6	2.2	1102	1	MYSC_CHICK	P29616	gallus gall	653	5	1.8	55	1	YHFG_ECOLI	P37770	escherichia
581	6	2.2	1103	1	CHS6_USTUA	O13395	ustilago ma	654	5	1.8	55	1	YHFG_SALTY	P37771	salmonella
582	6	2.2	1115	1	YAA4_SCHPO	Q09798	schizosacch	655	5	1.8	58	1	ATP6_BRATO	Q31721	brassica to
583	6	2.2	1121	1	YEO6_YEAST	P32644	saccharomyc	656	5	1.8	59	1	SAKA_LACSK	P80097	lactobacill
584	6	2.2	1182	1	RTP2_TRYBG	P15594	trypanosoma	657	5	1.8	60	1	HNEN_LAMPL	P15334	lampetra pl
585	6	2.2	1191	1	SMC2_MOUSE	Q8c948	mus musculus	658	5	1.8	60	1	RS14_MYCCA	P10130	mycoplasma
586	6	2.2	1193	1	YFBR_BACSU	P54159	bacillus su	659	5	1.8	60	1	YH05_VACCV	P17356	vaccinia vi
587	6	2.2	1197	1	SMC2_HUMAN	O95347	homo sapien	660	5	1.8	61	1	143X_MAIZE	P29306	zea mays (m
588	6	2.2	1203	1	SMC2_XENLA	P50533	xenopus lae	661	5	1.8	61	1	SUIS_PIG	P56729	sus scrofa
589	6	2.2	1214	1	SIP1_HUMAN	O60315	homo sapien	662	5	1.8	62	1	Y12D_BPT4	P39496	bacterioph
590	6	2.2	1215	1	SIP1_MOUSE	Q9r0g7	mus musculus	663	5	1.8	63	1	CE3G_HYPCU	P50723	hyphantria
591	6	2.2	1224	1	COPA_BOVIN	Q27954	bos taurus	664	5	1.8	63	1	COW3_CONTE	Q9nda6	conus texti
592	6	2.2	1248	1	TOPG_SULAC	Q08582	sulfolobus	665	5	1.8	63	1	COW_CONRA	P58786	conus radia
593	6	2.2	1265	1	RPOD_CYAPA	P48120	cyanophora	666	5	1.8	64	1	FABP_ACASI	O76821	acarus siro
594	6	2.2	1283	1	OSH2_YEAST	O12451	saccharomyc	667	5	1.8	64	1	PHYB_PHYBI	P81565	phyllomedus
595	6	2.2	1367	1	LT23_CABEL	P24348	caenorhabdi	668	5	1.8	66	1	YQ23_BACAN	Q9rn09	bacillus an
596	6	2.2	1416	1	BLM_MOUSE	O88700	mus musculus	669	5	1.8	67	1	CERC_CERCA	Q17313	ceratitis c
597	6	2.2	1427	1	ZFH2_SCHPO	Q9c0a1	homo sapien	670	5	1.8	67	1	CSPB_BACSU	P32081	bacillus su
598	6	2.2	1428	1	YAB4_SCHPO	Q09773	schizosacch	671	5	1.8	67	1	HM1_CHICK	P13544	gallus gall
599	6	2.2	1432	1	WRN_HUMAN	O14191	homo sapien	672	5	1.8	68	1	YOR3_FIVSD	P19031	feline immu
600	6	2.2	1436	1	WRN_XENLA	Q93530	xenopus lae	673	5	1.8	69	1	RM39_YEAST	P36533	saccharomyc
601	6	2.2	1451	1	AT7B_RAT	Q64535	rattus norv	674	5	1.8	70	1	Y05Q_BPT4	P13305	bacterioph
602	6	2.2	1460	1	N159_YEAST	P40477	saccharomyc	675	5	1.8	70	1	Y535_TREPA	O83546	treponema p
603	6	2.2	1462	1	AT7B_MOUSE	Q64446	mus musculus	676	5	1.8	71	1	YS30_RALSO	Q8xvk0	raistonia s
604	6	2.2	1478	1	BUD3_ASHGO	Q9hf61	ashbya goss	677	5	1.8	73	1	BB13_SCHCO	P78744	schizophyll
605	6	2.2	1559	1	STCJ_EMENI	Q00681	emeritella	678	5	1.8	73	1	GEPA_BACSU	O06721	bacillus su
606	6	2.2	1574	1	RPOC_AQUAE	O67763	aquifex aeo	679	5	1.8	73	1	IFI_CHLPN	Q9z9a8	chlamydia p
607	6	2.2	1576	1	RPOC_AQUAP	Q9x6y2	aquifex pyr	680	5	1.8	73	1	PEPC_PIG	P30879	sus scrofa
608	6	2.2	1581	1	PRRB_HUMAN	Q15648	h peroxisom	681	5	1.8	74	1	CIM_BPMU	P30046	bacterioph
609	6	2.2	1658	1	ITN2_MOUSE	Q9z0r6	mus musculus	682	5	1.8	74	1	HOLI_BPDP1	Q03978	bacterioph
610	6	2.2	1677	1	VIT_ACITR	Q90243	acipenser t	683	5	1.8	74	1	UL11_HSVEB	P28982	equine herp
611	6	2.2	1696	1	ITN2_HUMAN	Q9nzm3	homo sapien	684	5	1.8	74	1	Y11B_BPT4	P32281	bacterioph
612	6	2.2	1714	1	SVEP_DROME	P28668	drosophila	685	5	1.8	74	1	Y4HR_RHISN	P55482	rhizobium s
613	6	2.2	1739	1	DOTL_HUMAN	Q8tek3	homo sapien	686	5	1.8	74	1	YD97_CAMJE	Q9pmr0	campylobact
614	6	2.2	1744	1	TANA_XENLA	Q01550	xenopus lae	687	5	1.8	75	1	RL31_BRAJA	Q89ub0	bradyrhizob
615	6	2.2	1807	1	TSC2_HUMAN	P49815	homo sapien	688	5	1.8	76	1	ACP_OCELI	P80922	oceanospiri
616	6	2.2	1808	1	TENA_CHICK	P10039	gallus gall	689	5	1.8	76	1	CD24_MOUSE	P24807	mus musculus
617	6	2.2	1809	1	TSC2_RAT	P49816	rattus norv	690	5	1.8	76	1	RL31_CAUCR	Q9a3c9	caulobacter

P02567	caenorhabdi
P12845	caenorhabdi
P05661	drosophila
P02566	caenorhabdi
P12844	caenorhabdi
Q9dell3	gallus gall
Q66802	ebola virus
P13886	o'nyong-nyo
Q9y496	homo sapien
P21333	homo sapien
Q8td26	homo sapien
Q09666	homo sapien
P12823	d genome po
P29990	d genome po
P29991	d genome po
P07564	d genome po
P14340	d genome po
Q9y698	homo sapien
Q66431	dugbe virus
Q9nyq8	homo sapien
Q05470	bacillus su
P40803	bacillus su
P04114	homo sapien
Q96pk2	homo sapien
P80701	pseudomonas
Q45827	chloroflexu
P04842	ichia past
P27386	bacterioph
P80100	ectothiorho
P80101	ectothiorho
Q83333	treponema p
Q9v201	pyrococcus
O8tzi3	pyrococcus
O74105	pyrococcus
P40641	alligator m
P37770	escherichia
P37771	salmonella
Q31721	brassica to
P80097	lactobacill
P15334	lampetra pl
P10130	mycoplasma
P17356	vaccinia vi
P29306	zea mays (m
P56729	sus scrofa
P39496	bacterioph
P50723	hyphantria
Q9nda6	conus texti
P58786	conus radia
O76821	acarus siro
P81565	phyllomedus
Q9rn09	bacillus an
Q17313	ceratitis c
P32081	bacillus su
P13544	gallus gall
P19031	feline immu
P36533	saccharomyc
P13305	bacterioph
O83546	treponema p
Q8xvk0	raistonia s
P78744	schizophyll
O06721	bacillus su
Q9z9a8	chlamydia p
P30879	sus scrofa
P30046	bacterioph
Q03978	bacterioph
P28982	equine herp
P32281	bacterioph
P55482	rhizobium s
Q9pmr0	campylobact
Q89ub0	bradyrhizob
P80922	oceanospiri
P24807	mus musculus
Q9a3c9	caulobacter

691	5	1.8	76	1	TATA_PASMU	Q9ckd3	pasteurella	764	96	1	VE7_HPV24	P50782	human papill
692	5	1.8	77	1	ACP1_PSEAE	Q54439	pseudomonas	765	97	1	7E_DICDI	P15649	dictyosteli
693	5	1.8	77	1	ACP_PSESM	P90923	pseudomonas	766	97	1	CH10_ACEAC	Q8gbd3	acetobacter
694	5	1.8	77	1	EX75_CLOAB	Q97hd1	clostridium	767	97	1	YF51_HELPV	Q9zj67	helicobacte
695	5	1.8	78	1	TEGP_SVVD	O45446	simian vari	768	98	1	CYTA_HUMAN	P01040	homo sapien
696	5	1.8	78	1	ACP_XANAC	P58986	xanthomonas	769	98	1	FIXX_RHIME	P09822	thizobium m
697	5	1.8	78	1	ACP_XANAL	Q9ez11	xanthomonas	770	98	1	P531_MOUSE	P70399	mus musculus
698	5	1.8	78	1	RLX_PPAE	Q8ztu0	pyrobaculum	771	98	1	Z126_HUMAN	P35275	homo sapien
699	5	1.8	78	1	UGL1_AMEPV	P29819	amsacta moo	772	99	1	ARG2_PHAU	P32292	phaseolus a
700	5	1.8	79	1	CSNA_CHLIE	Q84647	chlorobium	773	99	1	HC14_HUMAN	P05114	homo sapien
701	5	1.8	79	1	RPOZ_THEMEA	Q9x214	thermotoga	774	99	1	PCP2_HUMAN	Q8iv41	homo sapien
702	5	1.8	79	1	TATA_HELPV	Q9zmb8	helicobacte	775	99	1	YI07_MICTU	Q50718	mycobacteri
703	5	1.8	79	1	YD21_CAEEL	O55088	helicobacte	776	100	1	HG14_BOVIN	P02336	bos taurus
704	5	1.8	80	1	YD21_CAEEL	O17811	caenorhabdi	777	100	1	URE3_BORBR	P06705	bordetella
705	5	1.8	80	1	RUXG_ARATH	P25063	homo sapien	778	100	1	URE3_LACFE	P26931	lactobacill
706	5	1.8	81	1	ATPL_CLOAB	O82221	arabidopsis	779	100	1	URE3_STRSL	Q55053	streptococc
707	5	1.8	81	1	RUXG_MEDSA	O08310	clostridium	780	100	1	YH74_ARCFU	O28520	archaeoglob
708	5	1.8	81	1	Y65_BPT3	P24715	medicago sa	781	101	1	TSHB_PHOSU	P11646	zea mays (m
709	5	1.8	81	1	CSGA_BACSU	P20329	bacterioph	782	101	1	URE3_UREPA	Q62590	phodopus su
710	5	1.8	82	1	S61B_ARATH	P34379	bacillus su	783	101	1	URE3_UREUR	Q56557	ureaplasma
711	5	1.8	82	1	Y070_METUA	P38389	methanococc	784	101	1	VNS7_CVFE3	P17274	ureaplasma
712	5	1.8	82	1	Y070_METUA	Q50373	methanococc	785	101	1	VNS7_CVFE3	O29102	archaeoglob
713	5	1.8	82	1	Y070_METUA	P19191	bacterioph	786	101	1	VNS7_CVFE3	P19742	feline infe
714	5	1.8	83	1	GVG2_HALNI	P14406	homo sapien	787	101	1	VP15_BPAPS	O9t1t3	bacterioph
715	5	1.8	83	1	Y405_ARCFU	P33960	halobacteri	788	102	1	IFPB_AGRU	O52514	agrobacteri
716	5	1.8	83	1	Y405_ARCFU	O29842	archaeoglob	789	102	1	RS10_CLOAB	Q37eh7	clostridium
717	5	1.8	83	1	Y405_ARCFU	P46132	escherichia	790	102	1	RS10_PLARO	P72232	human papill
718	5	1.8	83	1	Y405_ARCFU	O29748	archaeoglob	791	102	1	VE7_HPV19	P36822	human papill
719	5	1.8	84	1	HEFC_RAT	Q99mh3	rattus norv	792	102	1	VE7_HPV19	P08795	bacterioph
720	5	1.8	84	1	CY66_PETFA	P00108	petalonia f	793	102	1	VE7_HPV19	P08795	bacterioph
721	5	1.8	85	1	UG73_HSV6U	P24439	human herpe	794	103	1	CEAV_ECOLI	P25322	escherichia
722	5	1.8	85	1	UG73_HSV6U	Q52888	mycobacteri	795	103	1	EMF1_CHICK	P28317	gallus gall
723	5	1.8	86	1	CY66_ALAES	P00109	alarial escu	796	103	1	H1S2_RHOCH	Q50723	rhodobacter
724	5	1.8	86	1	CY66_BUMFI	P00110	bullerliop	797	103	1	H1S2_RHOCH	P50935	rhodobacter
725	5	1.8	87	1	ANSA_STRCZ	P01548	streptomyce	798	103	1	LAC_CHICK	P20763	gallus gall
726	5	1.8	87	1	HEB_DASVI	P07420	dasyurus vi	799	103	1	NRAW_IACAO	P26143	influenza a
727	5	1.8	87	1	NUOS_HUMAN	Q9nrx3	homo sapien	800	103	1	OST4_PIG	Q29381	sus scrofa
728	5	1.8	87	1	RS20_CORGL	Q9nn66	corynebacte	801	103	1	YCX2_CHLEP	P05721	chlorella p
729	5	1.8	87	1	RS20_NEIMA	Q9jgm6	neisseria m	802	104	1	VATF_THEVO	Q37cql	thermoplasm
730	5	1.8	87	1	Y230_METUA	Q37683	methanococc	803	104	1	Y4EB_RHISN	P55425	thizobium s
731	5	1.8	87	1	YAF2_BACLI	P36549	bacillus li	804	105	1	NO93_SOYBN	O29221	glycine max
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733	5	1.8	88	1	RPOZ_HAEIN	P43740	haemophilus	806	106	1	C07S_HUMAN	O60397	homo sapien
734	5	1.8	88	1	RS15_BORBU	O51744	borrelia bu	807	106	1	KACB_RABIT	P01839	oryctolagus
735	5	1.8	89	1	FLIQ_BUCAL	P57185	buchnera ap	808	106	1	KACB_RAT	P01835	rattus norv
736	5	1.8	89	1	NRAW_TAMEI	P03471	influenza a	809	106	1	KACB_HUMAN	P01834	homo sapien
737	5	1.8	89	1	SDP1_MOUSE	P40224	mus musculus	810	106	1	VATF_HALVO	Q48331	halobacteri
738	5	1.8	89	1	VP54_BPAPS	O9t1t4	bacterioph	811	106	1	Y547_RICPR	Q32d03	rickettsia
739	5	1.8	89	1	YF19_MYCTU	Q30588	mycobacteri	812	106	1	YB07_YEAST	P38284	saccharomyc
740	5	1.8	90	1	BAPL_DROME	Q9vlu0	drosophila	813	106	1	YVBB_VACCC	P20554	vaccinia vi
741	5	1.8	90	1	DMPM_FESP	P19731	pseudococc	814	107	1	YB11_BACHD	Q86c00	thizobium l
742	5	1.8	90	1	MOAD_SYNPF	Q86209	synchococc	815	107	1	YB11_BACHD	Q86c00	thizobium l
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744	5	1.8	90	1	Y071_METUA	Q60374	methanococc	817	108	1	GLPE_ECOLI	P09390	escherichia
745	5	1.8	90	1	YEAC_ECOLI	P76231	escherichia	818	108	1	GLPE_SALTY	Q8x1c6	salmonella
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752	5	1.8	93	1	RS16_CANTP	Q9kts4	canidatus	825	109	1	GLPM_YERPE	Q8zj13	yersinia pe
753	5	1.8	93	1	SDP1_FELCA	O62657	felis silve	826	109	1	S213_MOUSE	P52112	pseudomonas
754	5	1.8	93	1	IFPB_RHOCA	P42030	rhodobacter	827	109	1	YMW3_MYCTU	Q50690	mus musculus
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758	5	1.8	94	1	Y753_TREPA	O93774	treponema p	831	110	1	VCAD_LAMB	P01712	bacterioph
759	5	1.8	94	1	YQVY_BACSU	P34499	bacillus au	832	110	1	Y484_RICPR	Q32d62	rickettsia
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839 1.8 111 1 YU64\_XANAF O8pi34 xanthomonas  
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842 1.8 112 1 SCGG\_HAEIN P44713 haemophilus  
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844 1.8 112 1 THL\_CLODI P45362 clostridium  
845 1.8 112 1 YC83\_GALSU Q9msa1 galdieria s  
846 1.8 113 1 H38\_STYLE P81202 stylonychia  
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848 1.8 113 1 RBFA\_LACLC Q9x765 lactococcus  
849 1.8 113 1 Y068\_METMP Q9p9e9 methanococc  
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861 1.8 115 1 HV44\_MOUSE P01820 mus musculus  
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865 1.8 115 1 TIAP\_HUMAN O95411 homo sapien  
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867 1.8 115 1 TKN1\_RCBIT P16826 human cytom  
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872 1.8 115 1 YF88\_MYCTU P13424 drosophila  
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876 1.8 116 1 NU3M\_ONCKI P20687 oncorhynchu  
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884 1.8 116 1 TKNK\_MOUSE P50999 mus musculus  
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886 1.8 116 1 YJ57\_YEAST P47132 saccharomyc  
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888 1.8 117 1 NTPF\_ENTHR P43437 enterococcu  
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892 1.8 118 1 YRP3\_IRV6 P18307 chilo iride  
893 1.8 118 1 YRP4\_IRV6 P18308 chilo iride  
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900 1.8 119 1 RBFA\_LACLC Q8chg3 lactococcus  
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902 1.8 120 1 NEUB\_XENLA P43443 xenopus lae  
903 1.8 120 1 NU3C\_SYNY3 P19045 synechocyst  
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908 1.8 120 1 Y555\_PYRHO O59124 pyrococcus  
909 1.8 121 1 GLN2\_METMP P71525 methanococc

Q50787 methanobact  
P07458 macropus ru  
O32142 bacillus su  
O26145 methanobact  
Q97150 clostridium  
Q9tlu2 cyanidium c  
Q9v108 pyrococcus  
P44293 haemophilus  
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P10137 mycoplasma  
P17909 escherichia  
P75381 mycoplasma  
Q8uij2 agrobacteri  
P29580 methanobact  
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P59372 mycoplasma  
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P77415 escherichia  
Q58918 methanococc  
Q9hpi8 halobacteri  
P45809 erwinia amy  
Q92ge1 rhizobium m  
P43028 mus musculu  
P55020 synechococc  
P00947 comanonas t  
O51083 borrelia bu  
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Q8pyn2 methanosarc  
Q90986 gallus gall  
P41985 bos taurus  
Q9n0t2 equus cabal  
P55396 rhizobium s  
P21078 vaccinia vi  
O36075 helicobacte  
P76545 escherichia  
Q8tj03 methanosarc  
Q8pye0 methanosarc  
O51124 borrelia bu  
Q11106 caenorhabdi  
P02361 escherichia  
P44377 haemophilus  
Q9v6v3 drosophila  
P42631 escherichia  
P21051 vaccinia vi  
P33822 variola vir  
Q8kaa4 chlorobium  
Q9pqk9 ureaplasma  
P81048 hyalophora  
P52819 caenorhabdi  
P06651 aspergillus  
P46180 buchnera ap  
Q9cl44 pasteurella  
Q9knz8 vibrio chol  
Q87sz9 vibrio para  
Q8de54 vibrio vuln  
Q8zj98 yersinia pe  
P75450 mycoplasma  
O67445 aquifex aeo  
P45547 escherichia  
P20109 mus musculu  
P42203 rattus norv  
Q77135 zapronus t  
Q8xv26 raiastonia s  
Q9hiy0 thermoplas  
P26377 bos taurus  
Q9ike8 rattus norv  
O67469 aquifex aeo  
P76289 escherichia  
P40684 serratia ma  
P40282 plasmodium  
P19931 escherichia

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983 1.8 132 1 NRDI_AGRTS Q8J69 agrobacteri
984 1.8 132 1 RS8_XANAC Q8J63 xanthomonas
985 1.8 132 1 RS8_XANCP Q8J63 xanthomonas
986 1.8 132 1 Y254_MYCGF P47526 mycoplasma
987 1.8 133 1 Y4DO_EHISN P5414 rhizobium s
988 1.8 133 1 Y067_CABEL P34748 caenorhabdi
989 1.8 134 1 CRB2_BACHD Q9K819 bacillus ha
990 1.8 134 1 CYS_ANOCU Q31684 anoura caud
991 1.8 134 1 H3_VOLCA P08437 volvox cart
992 1.8 134 1 NRDI_YEREE Q8ZD66 agrobacteri
993 1.8 134 1 TRBC_AGRTU P54908 agrobacteri
994 1.8 134 1 V020_BPT5 P23541 bacterioph
995 1.8 134 1 VC05_VARV P34013 variola vir
996 1.8 135 1 H31_TETPY P15511 tetrahymena
997 1.8 135 1 H3_ACRFO P22843 acropora fo
998 1.8 135 1 H3_EUPCR P20543 euplotes cr
999 1.8 135 1 NRDI_BRUME Q8YBG9 bruceella me
1000 1.8 135 1 YF84_MYCPN P75196 mycoplasma
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ALIGNMENTS

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RESULT 1
LINK_PSEPA STANDARD; PRT; 250 AA.
ID LINK_PSEPA STANDARD; PRT; 250 AA.
RX STRAIN=UT26;
RA Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
RT "Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
RT dehydrogenase gene involved in the degradation of gamma-
RT hexachlorocyclohexane in Pseudomonas paucimobilis.";
RL J. Bacteriol. 176:3117-3125(1994).
CC -1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
CC (2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHQ). LINK IS NOT
CC ESSENTIAL TO GAMMA-HCH DEGRADATION.
CC -1- PATHWAY: Degradation of gamma-hexachlorocyclohexane.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC
CC EMBL; D23722; BAA04939.1; -
CC HSPSP; P19992; IHDC.
CC InterPro; IPR002198; ADH short.
CC Pfam; PF00106; adh short.1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NP BIND 9 34 NAD (BY SIMILARITY).
FT ACT SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 250 AA; 25492 MW; 8C52703FF767382CF CRC64;
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Query Match 4.4%; Score 12; DB 1; Length 250;

Best Local Similarity 100.0%; Pred. No. 0.00024;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 GKVALITGGASG 24  
DB 7 GKVALITGGASG 18

RESULT 2  
YWFD\_BACSU STANDARD; PRT; 255 AA.  
ID YWFD\_BACSU STANDARD; PRT; 255 AA.  
RX STRAIN=168;  
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,  
RA Hulio M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,  
RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,  
RA Rapoport G., Danchin A.,  
PT "Bacillus subtilis genome project: cloning and sequencing of the 97  
PT kb region from 325 degrees to 333 degrees.";  
RL [Mot. Microbiol. 10:371-384(1993)].  
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RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=95020537; PubMed=7934828;  
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,  
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RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,  
RA Rapoport G., Danchin A.,  
PT "Bacillus subtilis genome project: cloning and sequencing of the 97  
PT kb region from 325 degrees to 333 degrees.";  
RL [Mot. Microbiol. 10:371-384(1993)].  
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RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bextero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita K., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Balchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Pohl T.M., Portetalle D., Porwollik S., Prescott A.M.,  
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter K., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
RT subtilis.";  
RL Nature 390:249-256(1997).  
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.

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DR EMBL; X73124; CAA51638.1; -;  
 DR EMBL; Z99123; CAB15799.1; -;  
 DR PIR; S39737; S39737.  
 DR HSSP; P50162; IAB1.  
 DR InterPro; BG10628; ywfd.  
 DR InterPro; IPR002198; ADH short.  
 DR Pfam; PF00106; adh\_short\_1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Hypothetical protein; Oxidoreductase; Complete proteome.  
 FT NP\_BIND 11 33 NAD OR NADP (BY SIMILARITY).  
 FT ACT\_SITE 154 154 BY SIMILARITY.  
 SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BFB88C9B CRC64;

Query Match 3.7%; Score 10; DB 1; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGASGIG 26

Db 11 LITGASGIG 20

#### RESULT 3

HCD2 BOVIN  
 ID\_HCD2\_BOVIN STANDARD; PRT; 261 AA.  
 AC 002691;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).  
 GN HADH2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RA MEDLINE=97214648; PubMed=9061028;  
 RX Futura S., Kobayashi A., Miyazawa S., Hashimoto T.;  
 RT "Cloning and expression of cDNA for a newly identified isozyme of  
 RT bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into  
 RT mitochondria.";  
 RL Biochim. Biophys. Acta 1350:317-324(1997).  
 CC 1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC 1- SUBUNIT: Homotetramer (By similarity).  
 CC 1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC 1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.

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CC EMBL; AB002156; BAAL19510.1; -;  
 CC HSSP; O70351; 1B6W.  
 CC InterPro; IPR002198; ADH short.  
 CC Pfam; PF00106; adh\_short\_1.  
 CC PRINTS; PR00080; SDRFAMILY.  
 CC PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase; NAD; Mitochondrion.  
 FT NP\_BIND 12 37 NAD (BY SIMILARITY).

FT ACT\_SITE 168 168 BY SIMILARITY.  
 SQ SEQUENCE 261 AA; 27140 MW; 8C7572BGA9A49780 CRC64;

Query Match 3.7%; Score 10; DB 1; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 0.026;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGASG 24

Db 12 VALITGASG 21

#### RESULT 4

BPBH COMTE  
 ID\_BPBH\_COMTE STANDARD; PRT; 281 AA.  
 AC Q463B1; Q46376;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)  
 DE (Biphenyl-2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-  
 DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)  
 DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase) (B2,3D).  
 GN BPBH.  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Comamonas.  
 OX NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=B-356;  
 RX MEDLINE=96316386; PubMed=8702262;  
 RA Sylvestre M., Hurtubise Y., Barriault D., Bergeron J., Ahmad D.,  
 RT "Characterization of active recombinant 2,3-dihydro-2,3-  
 RT dihydroxybiphenyl dehydrogenase from Comamonas testosteroni B-356 and  
 RT sequence of the encoding gene (bphB).";  
 RL Appl. Environ. Microbiol. 62:2710-2715(1996).  
 RN [2]  
 RP SEQUENCE OF 1-15 FROM N.A.  
 RC STRAIN=B-356;  
 RX MEDLINE=97045812; PubMed=8890734;  
 RA Sylvestre M., Siros M., Hurtubise Y., Bergeron J., Ahmad D.,  
 RA Shareck F., Barriault D., Guillemette I., Juteau J.M.;  
 RT "Sequencing of Comamonas testosteroni strain B-356-  
 RT biphenyl/chlorobiphenyl dioxygenase genes: evolutionary relationships  
 RT among Gram-negative bacterial biphenyl dioxygenases.";  
 RL Gene 174:193-202(1996).  
 CC 1- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +  
 CC NAD(+) = biphenyl-2,3-diol + NADH.  
 CC 1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO  
 CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.  
 CC 1- SUBUNIT: Homotetramer.  
 CC 1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.

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CC EMBL; U57451; AAB18304.1; -;  
 CC EMBL; U47637; AAC44530.1; -;  
 CC PIR; PC4213; PC4213.  
 CC HSSP; P47227; 1BDB.  
 CC InterPro; IPR002198; ADH short.  
 CC Pfam; PF00106; adh\_short\_1.  
 CC PRINTS; PR00080; SDRFAMILY.  
 CC PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NP\_BIND 10 34 NAD (BY SIMILARITY).

```

FT ACT SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 281 AA; 29350 MW; D50A4CC9167A113E CRC64;

Query Match 3.7%; Score 10; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGGAGS 24
Db 7 VALITGGAGS 16

RESULT 5
GS39_BACSU STANDARD; PRT; 285 AA.
ID _GS39_BACSU STANDARD; PRT; 285 AA.
AC P80873; P96577;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE General stress protein 39 (GSP39) (EC 1.---).
GN YPAD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_
PP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
RL Bacillus subtilis genome.";
RN Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[2]
PP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
AZavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
BRoriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruchsi C.V., Caldwell B., Capuano V., Carter N.M.,
CHOI S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
DENIZOT F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
ENTIAN K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
FRITZ C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
GHIM S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
GUISeppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
HILBERT H., Holsappel S., Hosono S., Hulio T.Y., Itaya M., Jones L.,
JAZIS B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
KOBAYASHI Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
KURITA K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
LEE S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
MEDINA N., Mellado R.F., Mizuno M., Moestl D., Nakai S., Noback M.,
NOONE D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
PARRO V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
PRESECAN E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RIEGER M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
SATO T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
SEKIGUCHI J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
SOROKIN A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
TAKEUCHI M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
TOSATO V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
VIARI A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
WINTERS P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
YOSHIDA K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
[3]
PP SEQUENCE OF 1-29.
RC STRAIN=168 / 1558;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
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RT regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463 (1997).
CC -I- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
CC LIMITATION AND OXYGEN LIMITATION.
CC -I- SIMILARITY: belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
CC EMBL; AB001488; BAA19257.1; -.
CC DR EMBL; Z99106; CAB12226.1; -.
CC DR PIR; D69768; D69768.
CC DR HSP; P50162; LAE1.
CC DR Subtilisin; BG12052; ydad.
CC DR InterPro; IPR002198; ADH short.
CC DR Pfam; PF00106; adh short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH SHORT; 1.
CC KW Oxidoreductase; Heat shock; Complete proteome.
FT INIT MET 0
FT NP BIND 45 69 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 190 190 BY SIMILARITY.
FT CONFLICT 21 21 E -> G (IN REF. 3).
FT CONFLICT 26 26 P -> K (IN REF. 3).
FT SEQUENCE 285 AA; 30951 MW; 98A7EF096B2C9AAE CRC64;

Query Match 3.3%; Score 9; DB 1; Length 285;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITGG 21
Db 41 GKVALITGG 49

RESULT 6
YUXG_BACSU STANDARD; PRT; 689 AA.
ID YUXG_BACSU STANDARD; PRT; 689 AA.
AC P40747;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase yuxG (EC 1.---) (ORF2).
GN YUXG OR YULA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97419515; PubMed=9274030;
RA Oudega B., Koningsstein G., Rodrigues L., de Sales Ramon M.,
HILBERT H., Dusterhoft A., Pohl T.M., Weitzenecker T.;
RT "Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (trnB) and 284 degrees
(pai).";
RL Microbiology 143:2769-2774 (1997).
[2]
PP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
AZavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
BRoriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruchsi C.V., Caldwell B., Capuano V., Carter N.M.,
CHOI S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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GHIM S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
GUISeppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
HILBERT H., Holsappel S., Hosono S., Hulio T.Y., Itaya M., Jones L.,
JAZIS B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
KOBAYASHI Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
KURITA K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
LEE S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
MEDINA N., Mellado R.F., Mizuno M., Moestl D., Nakai S., Noback M.,
NOONE D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
PARRO V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
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RIEGER M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
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SEKIGUCHI J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
SOROKIN A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
TAKEUCHI M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
TOSATO V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
VIARI A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
WINTERS P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
YOSHIDA K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
[3]
PP SEQUENCE OF 1-29.
RC STRAIN=168 / 1558;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
```

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RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serrtor P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."; 249-256 (1997).
RL Nature 390:249-256 (1997).
RN [3]
RP SEQUENCE OF 1-49 FROM N.A.
RX STRAIN=168 / O11085;
RX MEDLINE=94245722; PubMed=8188684;
RA Haulon D.W., Ordal G.W.;
RT "Cloning and characterization of genes encoding methyl-accepting
RT chemotaxis proteins in Bacillus subtilis.";
RL J. Biol. Chem. 269:14038-14046 (1994).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
DR EMBL; Z93938; CAB07952.1; -;
DR EMBL; Z99119; CAB15100.1; -;
DR EMBL; Z99120; CAB15111.1; -;
DR EMBL; L29189; AAA20558.2; -;
DR PIR; H70024; H70024.
DR HSSP; P25529; 1PMC.
DR Subtilisin; BG10947; YuxG.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00596; Aldolase_II; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Hypothetical protein; Oxidoreductase; Complete proteome.
FT ACT_SITE 579 579 BY SIMILARITY.
SQ SEQUENCE 689 AA; 76020 MW; 8BA82FDC3EEDD0FD CRC64;

Query Match 3.3%; Score 9; DB 1; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITGA 22
Db 428 KVALITGA 436
|||||
KVALITGA 436

RESULT 7
KUDU_ERWCH
ID KUDU_ERWCH STANDARD; PRT; 253 AA.
AC Q05528;
```

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DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) (2-keto-3-
DE deoxygluconate oxidoreductase).
GN KUDU.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3937;
RX MEDLINE=92114798; PubMed=1766386;
RA Condemine G., Robert-Baudouy J.;
RT "Analysis of an Erwinia chrysanthemi gene cluster involved in pectin
RT degradation.";
RL Mol. Microbiol. 5:2191-2202 (1991).
CC -!- CATALYTIC ACTIVITY: 2-deoxy-D-gluconate + NAD(+) = 3-dehydro-2-
CC deoxy-D-gluconate + NADH.
CC -!- PATHWAY: Pectin degradation.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62073; CAA43989.1; -;
DR PIR; S17711; S17711.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 14 38 NAD (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 253 AA; 27275 MW; 59E9827DEA471F76 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITG 20
Db 10 GKVALITG 17
|||||
GKVALITG 17

RESULT 8
SORD_KLEPN
ID SORD_KLEPN STANDARD; PRT; 267 AA.
AC P37079;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140) (Glucitol-6-
DE phosphate dehydrogenase) (Ketosephosphate reductase).
GN SORD.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1033-SP14 / KAY2026;
RX MEDLINE=95035038; PubMed=7947968;
RA Wehmeier U.F., Lengeler J.W.;
RT "Sequence of the sor-operon for L-sorbose utilization from Klebsiella
```



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RT pneumoniae KAY2026. ";
RL Blochim. Biophys. Acta 1208:348-351 (1994).
RN [2]
RP MEDLINE=95380679; PubMed=7652212;
RA Raizer J., Reizer A., Sier M.H. Jr.;
RT "Sorbose-1-P reductase (SOR) and the glucitol-6-P dehydrogenase
RI (Sor) of the Klebsiella pneumoniae L-sorbose operon belong to the
RT zinc-dependent dehydrogenase family and the short chain alcohol
RL dehydrogenase family, respectively.";
RS Microbiol. 146:183-184 (1995).
CC -1- CATALYTIC ACTIVITY: D-sorbitol 6-phosphate + NAD(+) = D-fructose
CC 6-phosphate + NADH.
CC -1- PATHWAY: SORBITOL METABOLIC PATHWAY.
CC -1- SUBUNIT: Homotetramer (by similarity).
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC
DR EMBL; X66059; CA946856.1; -.
DR F01; S50186; S50186.
DR HSP; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD.
FT NP BIND 160 160 BY SIMILARITY.
FT ACT SITE 160 160
SQ SEQUENCE 267 AA; 29005 MW; 44A9C31964384DEC CRC64;

Query Match 2.9%; Score 8; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TGGAGGIG 26
Db 15 TGGAGGIG 22

RESULT 9
BPHB_PSEPS STANDARD; PRT; 275 AA.
AC P08694;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cis-2,3-dihydroxybiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)
DE (Biphenyl-2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-
DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)
DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).
GN BPHB.
OS Pseudomonas pseudoalcaligenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=330;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KF707;
RX MEDLINE=87083404; PubMed=3793719;
RA Furukawa K., Aizawa N., Miyazaki T.;
RT "Nucleotide sequence of the 2,3-dihydroxybiphenyl dioxygenase gene of
RI Pseudomonas pseudoalcaligenes.";
RL J. Bacteriol. 169:427-429 (1987).
CC -1- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +
CC NAD(+) = biphenyl-2,3-diol + NADH.

```

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CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC
DR EMBL; M15333; AAA25752.1; ALT_INIT.
DR HSP; P47227; IBD8.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NP BIND 9 33 BY SIMILARITY.
FT ACT SITE 153 153
SQ SEQUENCE 275 AA; 28726 MW; F32A4A870B47E566 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGGASG 24
Db 9 LITGGASG 16

RESULT 10
BPHB_BURCE STANDARD; PRT; 277 AA.
ID BPHB_BURCE
AC P47227;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)
DE (Biphenyl-2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-
DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)
DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).
GN BPHB.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LB400;
RX MEDLINE=93345822; PubMed=8344527;
RA Hofer B., Eltis L.D., Dowling D.N., Timmis K.N.;
RT "Genetic analysis of a Pseudomonas locus encoding a pathway for
RT biphenyl/polychlorinated biphenyl degradation.";
RL Gene 130:47-55 (1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=98318037; PubMed=9655331;
RA Huelsmeyer M., Hecht H.-J., Niefind K., Hofer B., Eltis L.D.,
RA Timmis K.N., Schomburg D.;
RT "Crystal structure of cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase
RT from a PCB degrader at 2.0-A resolution.";
RL Protein Sci. 7:1286-1293 (1998).
CC -1- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +
CC NAD(+) = biphenyl-2,3-diol + NADH.
CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC -----

DR EMBL; X66122; CAA46909.1; -;  
DR PIR; JN0814; JN0814.  
DR PDB; 1BD8; 12-NOV-97.  
DR InterPro; IPR002198; ADH short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; 3D-structure.  
FT NP\_BIND 9 33 NAD (BY SIMILARITY).  
FT ACT\_SITE 155 155 BY SIMILARITY.  
FT TURN 2 5  
FT STRAND 7 11  
FT TURN 12 14  
FT HELIX 16 27  
FT TURN 28 29  
FT STRAND 31 36  
FT HELIX 39 49  
FT HELIX 50 52  
FT STRAND 53 57  
FT TURN 60 61  
FT HELIX 63 77  
FT STRAND 82 84  
FT TURN 92 93  
FT HELIX 96 98  
FT TURN 101 103  
FT HELIX 104 115  
FT TURN 116 116  
FT HELIX 117 133  
FT TURN 134 134  
FT STRAND 136 140  
FT HELIX 143 145  
FT TURN 146 146  
FT TURN 148 149  
FT HELIX 153 173  
FT TURN 174 176  
FT STRAND 178 184  
FT HELIX 195 197  
FT TURN 209 213  
FT TURN 214 216  
FT TURN 218 219  
FT HELIX 225 228  
FT HELIX 230 236  
FT HELIX 238 241  
FT TURN 242 243  
FT STRAND 248 251  
FT HELIX 255 257  
FT TURN 267 268  
FT HELIX 269 273  
FT TURN 274 274  
SQ SEQUENCE 277 AA; 28901 MW; 00194120BD4E12D1 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGASG 24  
| | | | |  
Db 9 LITGASG 16

RESULT 11  
BPBH\_PSEPU STANDARD; PRT; 277 AA.  
ID\_BPBH\_PSEPU  
AC\_P72220; PRT; 277 AA.  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C1s-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)  
DE (biphenyl-2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-  
DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)  
DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).  
GN BPBH.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O083;  
RX MEDLINE=97457193; PubMed=9311131;  
RA Khan A.A., Wang R.F., Nawaz M.S., Cerniglia C.E.;  
RT "Nucleotide sequence of the gene encoding cis-biphenyl dihydrodiol  
RT dehydrogenase (bpbh) and the expression of an active recombinant His-  
RT tagged bpbh gene product from a PCB degrading bacterium, Pseudomonas  
RT putida O083.";  
RL FEMS Microbiol. Lett. 154:317-324(1997).  
CC -1- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +  
CC NAD(+) = biphenyl-2,3-diol + NADH.  
CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO  
CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.  
CC -1- SUBUNIT: Homotetramer (Probable).  
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.  
CC -----  
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CC -----

DR EMBL; Y07655; CAA68939.1; -;  
DR HSP; P47227; 1BD8.  
DR InterPro; IPR002198; ADH short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
FT NP\_BIND 9 33 NAD (BY SIMILARITY).  
FT ACT\_SITE 155 155 BY SIMILARITY.  
FT SEQUENCE 277 AA; 28907 MW; A7048159903BE527 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGASG 24  
| | | | |  
Db 9 LITGASG 16

RESULT 12  
GSHR\_BURCE STANDARD; PRT; 449 AA.  
ID\_GSHR\_BURCE  
AC\_P48639;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glutathione reductase (EC 1.6.1.7) (GR) (Grase).  
GN GOR.  
OS Burkholderia cepacia (Pseudomonas cepacia).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia.  
OX NCBI\_TaxID=292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AC1100;  
RX MEDLINE=95266809; PubMed=7538273;

RA Daubaras D.L., Hershberger C.D., Kitano K., Chakrabarty A.M.;  
 RT "sequence analysis of a gene cluster involved in metabolism of 2,4,5-  
 RL trichlorophenoxyacetic acid by Burkholderia cepacia AC100.";  
 CC Appl. Environ. Microbiol. 61:1279-1289(1995).  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + NADP(+) = glutathione  
 CC disulfide + NADPH.  
 CC -1- COFACTOR: FAD.  
 CC -1- PATHWAY: 2,4,5-trichlorophenoxyacetic acid degradation.  
 CC -1- SUBUNIT: Homodimer (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.  
 CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE  
 CC OXIDOREDUCTASES CLASS-I.  
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 CC -----  
 CC EMBL: U19883; AAC43334.1; -;  
 CC PIR: I40178; I40178.  
 CC HSP: P28593; IAOG.  
 CC InterPro: IPR001327; FAD\_Pyr\_redox.  
 CC InterPro: IPR006324; Glut\_reduct\_2.  
 CC InterPro: IPR000815; Hg\_reductase.  
 CC InterPro: IPR001100; Pyr\_redox.  
 CC InterPro: IPR004039; Pyr\_redox\_dlm.  
 CC Pfam: PF00070; Pyr\_redox; 1.  
 CC Pfam: PF02852; Pyr\_redox\_dlm; 1.  
 CC PRINTS: PR00368; FADPNR.  
 CC PRINTS: PR00945; HGRDTASE.  
 CC PRINTS: PR00411; PNDRTASEI.  
 CC ProDom: PD000139; FAD\_Pyr\_redox; 1.  
 CC TIGRfams: TIGR01424; Gluta\_reduc\_2; 1.  
 CC PROSITE: PS00076; PYRIDINE\_REDOX\_1; 1.  
 CC Redox-active center; Oxidoreductase; Flavoprotein; FAD; NADP.  
 CC NP\_BIND 7 37 FAD (ADP PART) (PROBABLE).  
 CC DLSULFID 43 48 REDOX-ACTIVE (BY SIMILARITY).  
 CC NP\_BIND 292 302 FAD (FLAVIN PART) (BY SIMILARITY).  
 CC ACT\_SITE 435 435 BY SIMILARITY.  
 CC ACT\_SITE 449 449 47541 MW; 402FCG6E7A8D6720 CRC64;  
 CC SEQUENCE 449 AA; 47541 MW; 402FCG6E7A8D6720 CRC64;  
 CC -----  
 CC Query Match 2.9%; Score 8; DB 1; Length 449;  
 CC Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Qy 36 HGAKVAIA 43  
 CC Db 27 HGAKVAIA 34  
 CC -----  
 CC RESULT 13  
 CC R27A SCHPO STANDARD; PRT; 136 AA.  
 CC ID R27A SCHPO  
 CC AC O14388; O74167;  
 CC DT 15-DEC-1998 (Rel. 37, Created)  
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE 60S RIBOSOMAL PROTEIN L27-A.  
 CC GN RPL27A OR SPAC695.07C  
 CC OS Schizosaccharomyces pombe (Fission yeast).  
 CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 CC OC Schizosaccharomyces.  
 CC OX NCBI\_TaxID=4896;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC RP STRAIN=972;  
 CC RX MEDLINE=21848401; PubMed=11859360;  
 CC RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayles J., Baker S., Bigham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gatties S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Mouton S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford O., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skellern J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Woldward J., Vanstreels E., Rieger M., Schaefer M., Hilbert H.,  
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambut V., Mottier S.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rechet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 RL [2]  
 RL SEQUENCE OF 1-74 FROM N.A.  
 RL STRAIN=972;  
 RL Jang Y.J., Yoo H.S.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RL SEQUENCE OF 4-136 FROM N.A.  
 RL Kawamukai M.;  
 RT "S.pombe ribosomal protein L27 homolog.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L27 IN S.POMBE.  
 CC -1- SIMILARITY: BELONGS TO THE L27E FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL: AL049474; CAB39364.1; -;  
 CC EMBL: U97385; AAB53877.1; -;  
 CC EMBL: AB015354; BAA28649.1; -;  
 CC PIR: T40638; T40638.  
 CC PIR: T43374; T43374.  
 CC GeneDB Spombe; SPBC695.07c; -;  
 CC InterPro: IPR005824; KOW.  
 CC InterPro: IPR006646; KOW\_sub.  
 CC InterPro: IPR001141; Ribosomal\_L27e.  
 CC Pfam: PF00467; KOW; 1.  
 CC Pfam: PF01777; Ribosomal\_L27e; 1.  
 CC ProDom: PD009396; Ribosomal\_L27e; 1.  
 CC SMART: SM00739; KOW; 1.  
 CC PROSITE: PS01107; RIBOSOMAL\_L27e; 1.  
 CC RIBOSOMAL PROTEIN, Multigene family.  
 CC CONFLICT 4 6 ILK -> GTR (IN REF. 3).  
 CC SEQUENCE 136 AA; 15389 MW; 3D5C1526AD501F72 CRC64;  
 CC -----  
 CC Query Match 2.6%; Score 7; DB 1; Length 136;  
 CC Best Local Similarity 100.0%; Pred. No. 16;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Qy 13 GKVALIT 19  
 CC Db 8 GKVALIT 14

```
RESULT 14
GLB2 ASCSU          STANDARD;          PRT;    153 AA.
AC P49672;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myoglobin (Globin, body wall isoform).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Body wall muscle;
RA MEDLINE=95074010; PubMed=7982924;
RX Blaxter M.L., Vanfleteren J.R., Xia J., Moens L.;
RT "Structural characterization of an Ascaris myoglobin.";
RL J. Biol. Chem. 269:30181-30186(1994).
CC -!- FUNCTION: HIGH OXYGEN AFFINITY. PROBABLY SUPPLIES OXYGEN NEEDED
CC FOR MUSCLE ACTIVITY.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: BODY WALL GLOBIN IS LOCALIZED IN CELLULAR
CC LATERAL CORDS, THE NERVE RING, AND BODY WALL MUSCLE.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: Belongs to the globin family.
CC -----
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CC -----
DR EMBL; U17337; AAA64695.1; -.
DR PIR; A55139; A55139.
DR HSSP; P28316; 1ASH.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; Globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT METAL 94
FT IRON (HEME PROXIMAL LIGAND)
FT (BY SIMILARITY)
SQ SEQUENCE 153 AA; 17454 MW; 1B3EF94A15B49B98 CRC64;

Query Match          2.6%; Score 7; DB 1; Length 153;
Best Local Similarity 100.0%; Pred.No.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 ALGKKFS 204
    |||||
Db 133 ALGKKFS 139

RESULT 15
QY5B_CAEEL
ID YQ5B_CAEEL          STANDARD;          PRT;    154 AA.
AC Q09254;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 15.4 kDa protein C16C10.11 in chromosome III.
GN C16C10.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
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RA Lloyd C.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; Z46787; CAA86749.1; -.
DR PIR; T19332; T19332.
DR WormPep; C16C10.11; CE01491.
DR InterPro; IPR007017; DUF657.
DR Pfam; PF04933; DUF657; 1.
KW Hypothetical protein.
SQ SEQUENCE 154 AA; 15388 MW; 5F5C618B637D2683 CRC64;

Query Match          2.6%; Score 7; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 GGGSSHA 161
    |||||
Db 90 GGGSSHA 96

Search completed: October 23, 2003, 13:03:11
Job time : 55 secs
```



OM protein - protein search, using sw model

Run on: October 23, 2003, 12:59:05 ; Search time 96 Seconds  
(without alignments)  
733.837 Million cell upd

Title: US-09-673-918A-2  
Perfect score: 273  
Sequence: 1 MQLRTAFARRLEGKVALITG.....IDGGFVCNSVIKVFQYPS 273

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 1000 summaries

```
Database :
SPTRMBWL_23.*
1:  sp.arched.*
2:  sp.bacteria.*
3:  sp.fungi.*
4:  sp.human.*
5:  sp.invertebrate.*
6:  sp.mammal.*
7:  sp.mhc.*
8:  sp.organella.*
9:  sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertebrate.*
14: sp.unclassified.*
15: sp.rvirus.*
16: sp.bacteriap.*
17: sp.archeap.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description.
		Match	%				
1	110	40.3	277	10	Q94KL7	Q94KL7	forssythia i
2	17	6.2	234	10	Q40590	Q40590	nicotiana t
3	17	6.2	284	10	O50038	O50038	nicotiana t
4	16	5.9	283	10	Q3ZR17	Q3ZR17	arabidopsis
5	14	5.1	306	10	Q34184	Q34184	arabidopsis
6	14	5.1	306	10	Q9LW34	Q9LW34	arabidopsis
7	13	4.8	267	10	P93697	P93697	vigna ungu
8	13	4.8	274	10	Q8HD09	Q8HD09	phaseolus l
9	13	4.8	321	10	Q8LI04	Q8LI04	oryza sativ
10	12	4.4	160	10	Q8S987	Q8S987	ipomoea tri
11	12	4.4	277	10	Q3SBD7	Q3SBD7	ipomoea tri
12	12	4.4	277	10	Q3SBD8	Q3SBD8	ipomoea tri
13	12	4.4	284	10	Q3SBD6	Q3SBD6	ipomoea tri
14	12	4.4	284	10	O82465	O82465	ipomoea tri
15	11	4.0	278	3	P87017	P87017	aspergillus
16	11	4.0	278	3	Q8J2U8	Q8J2U8	aspergillus

90	8	2.9	263	16	Q9RJV4	Q9xlv4 streptomyce	163	7	2.6	250	2	Q8GDE6	Q8gde6 pseudomonas
91	8	2.9	268	10	Q9SOP9	Q9aqf9 pium sativ	164	7	2.6	251	2	Q9F7E0	Q9f7e0 acinetobact
92	8	2.9	268	10	Q9SQJ3	Q9sqj3 pium sativ	165	7	2.6	251	5	Q9VS71	Q9vs71 drosophila
93	8	2.9	268	16	Q8X5Z2	Q8x5z2 escherichia	166	7	2.6	251	10	Q40133	Q40133 lycopersico
94	8	2.9	268	16	Q8FPA9	Q8fb49 escherichia	167	7	2.6	251	16	Q8PR00	Q8pr00 xanthomonas
95	8	2.9	271	2	Q23136	Q23136 clostridium	168	7	2.6	251	16	Q8PE31	Q8pe31 xanthomonas
96	8	2.9	272	2	Q9LC88	Q9lcs8 nocardioide	169	7	2.6	252	4	Q56HD5	Q56hd5 homo sapien
97	8	2.9	276	2	Q9L748	Q9l748 pseudomonas	170	7	2.6	252	16	Q8CQ73	Q8cq73 staphylococ
98	8	2.9	276	2	Q9S570	Q9s570 pseudomonas	171	7	2.6	252	17	Q9YC93	Q9yc93 aeropyrum p
99	8	2.9	277	2	Q8AEY1	Q8aey1 pseudomonas	172	7	2.6	253	16	Q8XPA8	Q8xpa8 clostridium
100	8	2.9	277	2	Q8S287	Q8s287 sphingomona	173	7	2.6	253	16	Q8EMX3	Q8emx3 oceanobacil
101	8	2.9	277	2	Q8S2030	Q8s2030 pseudomonas	174	7	2.6	255	16	P95286	P95286 mycobacteri
102	8	2.9	278	16	Q9RW1	Q9rwd5 deinoococcus	175	7	2.6	255	16	Q92RM7	Q92rm7 rhizobium m
103	8	2.9	279	5	Q9XTD5	Q9xtd5 caenorhabdi	176	7	2.6	255	16	Q9L2C9	Q9l2c9 streptomyce
104	8	2.9	285	16	Q8YLW4	Q8ylw4 anabaena sp	177	7	2.6	257	16	Q983U4	Q983u4 rhizobium l
105	8	2.9	286	3	Q9HE38	Q9he38 neurospora	178	7	2.6	257	16	Q8UBE2	Q8ube2 agrobacteri
106	8	2.9	287	16	Q987Y1	Q987y1 rhizobium l	179	7	2.6	258	16	Q8PG10	Q8pg10 xanthomonas
107	8	2.9	289	16	Q8CN03	Q8cn03 staphylococ	180	7	2.6	258	16	Q8P4E8	Q8p4e8 xanthomonas
108	8	2.9	295	2	P94129	P94129 acinetobact	181	7	2.6	258	16	Q8EN56	Q8en56 oceanobacil
109	8	2.9	296	16	Q9ABX6	Q9abx6 caulobacter	182	7	2.6	259	10	Q9LEG3	Q9leg3 lycopersico
110	8	2.9	299	16	Q97J63	Q97j63 clostridium	183	7	2.6	259	16	Q98GY6	Q98gy6 rhizobium l
111	8	2.9	319	10	Q9SK30	Q9sk30 arabidopsis	184	7	2.6	260	16	Q98H11	Q98h11 rhizobium l
112	8	2.9	321	10	Q9LG18	Q9lg18 oryza sativ	185	7	2.6	261	16	Q9PEW5	Q9pew5 xylella fas
113	8	2.9	331	16	Q8GGG9	Q8ggg9 rhizobium l	186	7	2.6	261	16	Q9ABI1	Q9abi1 caulobacter
114	8	2.9	391	16	Q8PES3	Q8pes3 xanthomonas	187	7	2.6	261	16	Q987X7	Q987x7 rhizobium l
115	8	2.9	424	16	Q8F8H1	Q8feh1 corynebacte	188	7	2.6	261	16	Q8UES6	Q8ues6 agrobacteri
116	8	2.9	629	10	Q9FX95	Q9fx95 arabidopsis	189	7	2.6	261	16	Q8UES6	Q8ues6 agrobacteri
117	8	2.9	629	10	Q9J174	Q9j174 arabidopsis	190	7	2.6	263	16	Q8D564	Q8d564 yersinia pe
118	8	2.9	657	16	P73359	P73359 synchocyst	191	7	2.6	264	16	Q8U713	Q8u713 rhizobium m
119	8	2.9	36	3	Q14387	Q14387 schizosacch	192	7	2.6	267	16	Q92BP4	Q92bp4 rhizobium m
120	7	2.6	95	3	Q9YH7	Q9yh7 pitomyces s	193	7	2.6	269	2	Q9AQNS	Q9aqs pseudomonas
121	7	2.6	107	16	Q8XK08	Q8xk08 clostridium	194	7	2.6	269	2	Q8GI30	Q8gi30 pseudomonas
122	7	2.6	111	16	Q8VJ57	Q8vj57 mycobacteri	195	7	2.6	269	2	Q8GI30	Q8gi30 pseudomonas
123	7	2.6	111	17	Q9YD33	Q9yd33 aeropyrum p	196	7	2.6	271	16	Q8U612	Q8u612 agrobacteri
124	7	2.6	118	10	Q9FZ02	Q9fz02 cucumis sat	197	7	2.6	274	16	Q8KBL5	Q8kbl5 chlorobium
125	7	2.6	132	16	Q8F268	Q8f268 leptospira	198	7	2.6	275	16	Q8E9H5	Q8eh5 shewanella
126	7	2.6	133	11	Q8BBS3	Q8bbg3 mus musculu	199	7	2.6	281	17	Q92061	Q92061 archaeoglob
127	7	2.6	141	17	Q9VE51	Q9ve51 aeropyrum p	200	7	2.6	282	11	Q9D3M7	Q9d3m7 mus musculu
128	7	2.6	146	17	Q58420	Q58420 pyrococcus	201	7	2.6	282	13	Q73678	Q73678 oryzias lat
129	7	2.6	159	16	Q9H233	Q9hz23 pseudomonas	202	7	2.6	286	10	Q9C7L3	Q9c7l3 arabidopsis
130	7	2.6	162	2	Q9L768	Q9l768 deaulyovibr	203	7	2.6	286	16	Q9I1X3	Q9i1x3 pseudomonas
131	7	2.6	165	10	Q8W5E3	Q8w5e3 oryza sativ	204	7	2.6	287	10	Q8LID2	Q8lid2 oryza sativ
132	7	2.6	172	16	Q9RT56	Q9rt56 deinoococcus	205	7	2.6	289	15	Q893K6	Q893k6 streptomyce
133	7	2.6	181	16	Q9RVH8	Q9rvh8 deinoococcus	206	7	2.6	289	15	Q89399	Q89399 walleye der
134	7	2.6	183	2	Q9T41	Q9t41 bacillus an	207	7	2.6	298	10	Q9LTV6	Q9ltv6 arabidopsis
135	7	2.6	188	16	Q8XEW8	Q8xew8 salmonella	208	7	2.6	300	16	Q8XV19	Q8xv19 ralstonia s
136	7	2.6	190	2	Q9AGH5	Q9agn5 klebsiella	209	7	2.6	306	10	Q8LIC2	Q8lic2 oryza sativ
137	7	2.6	191	17	Q29904	Q29904 archaeoglob	210	7	2.6	308	16	Q8XRP5	Q8xrp5 ralstonia s
138	7	2.6	200	10	Q80711	Q80711 arabidopsis	211	7	2.6	308	16	Q8CU92	Q8cu92 staphylococ
139	7	2.6	203	16	Q8E028	Q8e028 streptococ	212	7	2.6	315	6	Q95JF5	Q95jf5 oryctolagus
140	7	2.6	207	5	Q44951	Q44951 caenorhabdi	213	7	2.6	316	10	Q8LIB9	Q8lib9 oryza sativ
141	7	2.6	215	3	Q60171	Q60171 schizosacch	214	7	2.6	316	10	Q8LIB8	Q8lib8 oryza sativ
142	7	2.6	217	16	Q9I7B3	Q9i7b3 pseudomonas	215	7	2.6	317	5	Q9VRJ4	Q9vrj4 drosophila
143	7	2.6	217	16	Q8E5R1	Q8e5r1 streptococ	216	7	2.6	323	16	Q8YLA8	Q8yla8 anabaena sp
144	7	2.6	222	2	Q24831	Q24831 acinetobact	217	7	2.6	328	16	Q914J8	Q914j8 pseudomonas
145	7	2.6	229	2	Q53064	Q53064 rhodococcus	218	7	2.6	328	16	P72043	P72043 mycobacteri
146	7	2.6	231	4	Q07985	Q07985 homo sapien	219	7	2.6	329	2	Q93PV9	Q93pv9 selenomonas
147	7	2.6	232	16	Q9PA83	Q9pa83 xylella fas	220	7	2.6	331	16	Q8KH47	Q8kh47 clostridium
148	7	2.6	232	16	Q9BJ95	Q9bj95 rhizobium l	221	7	2.6	336	2	Q56866	Q56866 yersinia en
149	7	2.6	233	8	Q9BRW3	Q9brw3 guillardia	222	7	2.6	339	8	Q36443	Q36443 mycena galo
150	7	2.6	233	12	Q9L1E2	Q9lie2 lymantria d	223	7	2.6	339	16	Q8Y339	Q8y339 anabaena sp
151	7	2.6	239	16	Q8RD37	Q8rd97 thermoaer	224	7	2.6	340	17	Q8TRK1	Q8trk1 methanosarc
152	7	2.6	242	2	Q8AP13	Q8ap19 methylobact	225	7	2.6	346	2	Q9X2W9	Q9x2w9 rhodospiril
153	7	2.6	243	16	Q8RG25	Q8rg25 fusobacteri	226	7	2.6	346	5	Q9VEB6	Q9veb6 drosophila
154	7	2.6	244	2	Q8VLS3	Q8vls3 xanthobacte	227	7	2.6	353	5	Q961E1	Q961e1 drosophila
155	7	2.6	245	16	Q8YFP3	Q8yfp3 bruceella me	228	7	2.6	353	16	Q8XU83	Q8xu83 ralstonia s
156	7	2.6	245	16	Q8G271	Q8g271 bruceella su	229	7	2.6	355	16	Q92N16	Q92n16 rhizobium m
157	7	2.6	246	16	Q8ZFW2	Q8zfw2 yersinia pe	230	7	2.6	357	5	Q7370	Q7370 plasmid
158	7	2.6	247	2	Q9JRM0	Q9jrm0 acinetobact	231	7	2.6	362	16	Q9R966	Q9r966 bruceella me
159	7	2.6	248	16	Q8ZG59	Q8zgs9 yersinia pe	232	7	2.6	362	16	Q8G219	Q8g219 bruceella su
160	7	2.6	248	16	Q8U9R1	Q8u9r1 agrobacteri	233	7	2.6	365	3	Q9HDU4	Q9hd4 schizosacch
161	7	2.6	249	5	Q9W4U2	Q9w4u2 drosophila	234	7	2.6	366	2	Q8KJ53	Q8kj53 rhizobium l
162	7	2.6	249	15	Q9J6W7	Q9j6w7 human immu	235	7	2.6	366	16	Q98AU5	Q98au5 rhizobium l

236	7	2.6	369	13	Q8AV11	Q8av11 xenopus lae	309	7	2.6	824	4	Q8N719	Q8n719 homo sapien
237	7	2.6	372	2	Q8VQ49	Q8vq49 escherichia	310	7	2.6	830	4	Q8WVC5	Q8wvc5 homo sapien
238	7	2.6	372	2	Q93Q33	Q93q33 salmonella	311	7	2.6	872	2	Q47114	Q47114 escherichia
239	7	2.6	372	2	Q9S522	Q9s522 escherichia	312	7	2.6	902	5	O16161	O16161 mytilus edu
240	7	2.6	372	11	Q8K0C9	Q8k0c9 mus musculus	313	7	2.6	908	16	Q912W3	Q912w3 pseudomonas
241	7	2.6	372	11	Q8K3X3	Q8k3x3 cricetus	314	7	2.6	913	5	Q8T3E5	Q8t3e5 caenorhabdi
242	7	2.6	372	16	Q8S339	Q8s339 escherichia	315	7	2.6	928	2	Q8RT68	Q8rt68 bartonella
243	7	2.6	373	16	Q8Z5H1	Q8z5h1 salmonella	316	7	2.6	928	5	Q19128	Q19128 caenorhabdi
244	7	2.6	373	16	Q9F7A4	Q9f7a4 salmonella	317	7	2.6	938	11	Q8BK52	Q8bk52 mus musculus
245	7	2.6	377	2	Q9LA94	Q9la94 aeromonas h	318	7	2.6	946	2	P70888	P70888 bacteroides
246	7	2.6	377	10	Q9M7I6	Q9m7i6 zea mays (m	319	7	2.6	955	5	Q8MO86	Q8mo86 caenorhabdi
247	7	2.6	377	17	Q8Q087	Q8q087 methanosarc	320	7	2.6	960	10	Q8L671	Q8l671 oryza sativ
248	7	2.6	377	17	Q8P1P5	Q8p1p5 methanosarc	321	7	2.6	975	5	Q9NK78	Q9nkc78 leishmania
249	7	2.6	377	17	Q8PW64	Q8pw64 methanosarc	322	7	2.6	1024	11	Q8VDN3	Q8vdn3 mus musculus
250	7	2.6	377	17	Q8PRR5	Q8pr5 methanosarc	323	7	2.6	1039	16	Q8G4Q1	Q8g4q1 bifidobacte
251	7	2.6	380	10	Q94DC9	Q94dc9 oryza sativ	324	7	2.6	1052	17	Q8P2R1	Q8p2r1 methanosarc
252	7	2.6	383	5	Q9G231	Q9gz31 trypanosoma	325	7	2.6	1088	16	Q8EDG6	Q8edg6 shewanella
253	7	2.6	384	5	Q8T8N2	Q8t8n2 caenorhabdi	326	7	2.6	1092	16	Q8EFB4	Q8efb4 rhizobium l
254	7	2.6	386	4	Q8WXJ0	Q8wxj0 homo sapien	327	7	2.6	1107	3	Q12271	Q12271 saccharomyc
255	7	2.6	390	5	Q9TXJ3	Q9txj3 leishmania	328	7	2.6	1291	16	Q9KUU5	Q9kuu5 vibrio chol
256	7	2.6	390	17	Q9HNB6	Q9hnb6 halobacteri	329	7	2.6	1417	10	Q9FJQ9	Q9fjg9 arabidopsis
257	7	2.6	395	5	Q8T3U5	Q8t3u5 drosophila	330	7	2.6	1469	5	Q9V953	Q9v953 drosophila
258	7	2.6	395	10	Q65502	Q65502 arabidopsis	331	7	2.6	1530	11	Q9WUG5	Q9wug5 rattus norv
259	7	2.6	399	5	Q8T8N3	Q8t8n3 caenorhabdi	332	7	2.6	1778	16	Q8FA32	Q8fa32 listeria mo
260	7	2.6	399	16	Q8UEQ8	Q8ueq8 agrobacteri	333	7	2.6	1784	12	Q8Y515	Q8y515 norwalk vir
261	7	2.6	399	16	Q8KFR7	Q8kfr7 chlorobium	334	7	2.6	1787	12	Q8JXJ1	Q8jxj1 norwalk-lik
262	7	2.6	422	5	Q8SXL8	Q8sxl8 drosophila	335	7	2.6	2691	4	Q8NSJ2	Q8nsj2 homo sapien
263	7	2.6	422	5	Q9VVL0	Q9vvl0 drosophila	336	7	2.6	2692	4	Q9Y503	Q9y503 homo sapien
264	7	2.6	425	17	Q97W07	Q97w07 sulfolobus	337	7	2.6	2705	4	Q95303	Q95303 homo sapien
265	7	2.6	428	2	Q9APH0	Q9aph0 leptospira	338	7	2.6	2725	4	Q9NYE5	Q9nye5 homo sapien
266	7	2.6	428	16	Q8F225	Q8f225 leptospira	339	6	2.2	11	3	Q9C1R7	Q9c1r7 saccharomyc
267	7	2.6	431	16	Q9RSE0	Q9rse0 deinococcus	340	6	2.2	12	3	Q8J0A7	Q8j0a7 saccharomyc
268	7	2.6	436	5	Q95Y86	Q95y86 caenorhabdi	341	6	2.2	16	3	Q8J1R1	Q8j1r1 saccharomyc
269	7	2.6	444	16	Q9A4U2	Q9a4u2 caulobacter	342	6	2.2	20	3	Q8J1R0	Q8j1r0 saccharomyc
270	7	2.6	451	16	Q9I4N1	Q9i4n1 pseudomonas	343	6	2.2	27	12	Q8QSK5	Q8qsk5 hepatitis c
271	7	2.6	462	10	Q8LIC1	Q8lic1 oryza sativ	344	6	2.2	27	12	Q8QSK0	Q8qsk0 hepatitis c
272	7	2.6	466	16	Q9PKH7	Q9pkh7 chlamydia m	345	6	2.2	27	12	Q8QSK6	Q8qsk6 hepatitis c
273	7	2.6	466	16	Q9K671	Q9k671 bacillus ha	346	6	2.2	27	12	Q8QSK8	Q8qsk8 hepatitis c
274	7	2.6	470	2	Q30326	Q30326 acetobacter	347	6	2.2	27	12	Q8QSKJ1	Q8qskj1 hepatitis c
275	7	2.6	502	16	Q8YB45	Q8yb45 brucella me	348	6	2.2	27	12	Q8QSK3	Q8qsk3 hepatitis c
276	7	2.6	502	16	Q8FX93	Q8fx93 brucella su	349	6	2.2	27	12	Q8QSKJ0	Q8qskj0 hepatitis c
277	7	2.6	515	16	Q9KBJ3	Q9kbj3 bacillus ha	350	6	2.2	27	12	Q8QSK19	Q8qsk19 hepatitis c
278	7	2.6	519	16	Q8XJ44	Q8xj44 clostridium	351	6	2.2	27	12	Q8QSKJ9	Q8qskj9 hepatitis c
279	7	2.6	528	3	Q9C2B7	Q9c2b7 neospora	352	6	2.2	27	12	Q8QSK6	Q8qsk6 hepatitis c
280	7	2.6	532	10	Q9LKT4	Q9lkt4 arabidopsis	353	6	2.2	27	12	Q8QSKJ5	Q8qskj5 hepatitis c
281	7	2.6	533	5	Q8T996	Q8t996 drosophila	354	6	2.2	27	12	Q8QSKJ8	Q8qskj8 hepatitis c
282	7	2.6	544	16	Q9FCG8	Q9fcg8 streptomyce	355	6	2.2	27	12	Q8QSKJ7	Q8qskj7 hepatitis c
283	7	2.6	550	5	Q9Y141	Q9y141 drosophila	356	6	2.2	27	12	Q8QSKJ3	Q8qskj3 hepatitis c
284	7	2.6	554	10	Q9LU28	Q9lu28 arabidopsis	357	6	2.2	27	12	Q8QSK2	Q8qsk2 hepatitis c
285	7	2.6	557	10	Q9FEB7	Q9feb7 oryza sativ	358	6	2.2	27	12	Q8QSKJ4	Q8qskj4 hepatitis c
286	7	2.6	564	10	Q8RXV6	Q8rxv6 arabidopsis	359	6	2.2	27	12	Q8QSKJ2	Q8qskj2 hepatitis c
287	7	2.6	571	16	Q8ZLH0	Q8zlh0 salmonella	360	6	2.2	28	11	Q9QXB4	Q9qxb4 mus musculu
288	7	2.6	586	16	Q98LB3	Q98lb3 rhizobium l	361	6	2.2	33	12	Q72996	Q72996 hepatitis c
289	7	2.6	592	4	Q9UJT2	Q9ujt2 homo sapien	362	6	2.2	33	12	Q72995	Q72995 hepatitis c
290	7	2.6	601	16	Q9HYI2	Q9hyi2 pseudomonas	363	6	2.2	33	12	Q72997	Q72997 hepatitis c
291	7	2.6	609	3	Q9HFY2	Q9hfy2 neospora	364	6	2.2	33	12	Q72999	Q72999 hepatitis c
292	7	2.6	634	5	Q9V978	Q9v978 drosophila	365	6	2.2	33	12	Q72998	Q72998 hepatitis c
293	7	2.6	634	5	Q44116	Q44116 drosophila	366	6	2.2	33	12	Q72994	Q72994 hepatitis c
294	7	2.6	643	2	Q68085	Q68085 rhodobacter	367	6	2.2	33	12	Q73007	Q73007 hepatitis c
295	7	2.6	659	16	Q8FTU7	Q8ftu7 corynebacte	368	6	2.2	33	12	Q73004	Q73004 hepatitis c
296	7	2.6	677	10	Q9FNB7	Q9fnb7 arabidopsis	369	6	2.2	36	2	Q9R4X9	Q9r4x9 azotobacter
297	7	2.6	679	10	Q8GY46	Q8gy46 arabidopsis	370	6	2.2	37	2	Q8KKA8	Q8kka8 proteus vul
298	7	2.6	693	10	Q9FTM8	Q9ftm8 arabidopsis	371	6	2.2	40	12	Q91K62	Q91k62 hepatitis c
299	7	2.6	717	16	Q92NM8	Q92nm8 rhizobium m	372	6	2.2	41	16	Q987D0	Q987d0 rhizobium l
300	7	2.6	724	16	Q8UDN9	Q8udn9 agrobacteri	373	6	2.2	43	6	Q9XSR9	Q9xsr9 canis famil
301	7	2.6	790	2	Q9X285	Q9x285 pantoea cit	374	6	2.2	45	12	Q9PXQ4	Q9pxq4 hepatitis c
302	7	2.6	792	16	Q8GIM8	Q8gim8 brucella su	375	6	2.2	46	17	Q8U113	Q8u113 pyrococcus
303	7	2.6	796	16	Q8ZRS1	Q8zrs1 salmonella	376	6	2.2	47	12	Q9QK97	Q9qk97 rift valley
304	7	2.6	796	16	Q8Z9E0	Q8z9e0 salmonella	377	6	2.2	47	12	Q9QK94	Q9qk94 rift valley
305	7	2.6	796	16	Q8X946	Q8x946 escherichia	378	6	2.2	47	12	Q9QK90	Q9qk90 rift valley
306	7	2.6	797	16	Q8Y9G6	Q8y9g6 brucella me	379	6	2.2	47	12	Q9QK93	Q9qk93 rift valley
307	7	2.6	802	16	Q8FL38	Q8fl38 escherichia	380	6	2.2	47	12	Q9QKA0	Q9qka0 rift valley
308	7	2.6	823	16	Q8X287	Q8x287 escherichia	381	6	2.2	47	12	Q9QK96	Q9qk96 rift valley





528	6	2.2	119	17	Q8U0N0	Q8u0n0 pyrococcus	601	6	2.2	130	17	Q9YD79	Q9yd79 aeropyrum p
529	6	2.2	120	6	Q8HY50	Q8hy50 oryctolagus	602	6	2.2	132	10	Q9FUI9	Q9fui9 rubus idaeu
530	6	2.2	120	10	Q9AT96	Q9at96 brassica ca	603	6	2.2	132	16	Q8DS27	Q8ds27 streptococ
531	6	2.2	120	11	Q8C8D4	Q8c8d4 mus musculu	604	6	2.2	133	2	Q8KVS3	Q8kvs3 renibacteri
532	6	2.2	120	12	Q67426	Q67426 dengue viru	605	6	2.2	133	2	Q8KVS2	Q8kvs2 renibacteri
533	6	2.2	120	16	Q8UD03	Q8ud03 agrobacteri	606	6	2.2	133	16	Q922J1	Q922j1 rhizobium m
534	6	2.2	121	5	Q95SM4	Q95sm4 drosophila	607	6	2.2	133	17	Q9YDU6	Q9ydu6 aeropyrum p
535	6	2.2	122	11	Q9D105	Q9d105 mus musculu	608	6	2.2	133	17	Q9Y928	Q9y928 aeropyrum p
536	6	2.2	123	2	Q8GQ77	Q8gq77 pseudomonas	609	6	2.2	134	16	Q8YKA3	Q8yka3 anabaena sp
537	6	2.2	123	10	Q9LVR8	Q9lvr8 arabidopsis	610	6	2.2	134	17	O58583	O58583 pyrococcus
538	6	2.2	123	10	Q9XFM3	Q9xfm3 dianthus ca	611	6	2.2	136	2	O33929	O33929 staphylococ
539	6	2.2	123	16	Q9JQZ2	Q9jqz2 neisseria m	612	6	2.2	136	10	Q9FX60	Q9fx60 arabidopsis
540	6	2.2	123	16	Q99Z15	Q99z15 streptococ	613	6	2.2	136	10	Q8LCA8	Q8lca8 arabidopsis
541	6	2.2	123	16	Q8K6W0	Q8k6w0 streptococ	614	6	2.2	136	10	Q8SA80	Q8sa80 cryza sativ
542	6	2.2	124	2	Q9X563	Q9x563 enterococcu	615	6	2.2	137	10	Q9FX17	Q9fx17 arabidopsis
543	6	2.2	124	17	Q8QOM4	Q8qom4 methanosarc	616	6	2.2	137	12	O65517	O65517 barnah fore
544	6	2.2	125	17	Q97WY5	Q97wy5 sulfobolus	617	6	2.2	137	12	O28267	O28267 archaeoglob
545	6	2.2	126	2	P948Z5	P948z5 helicobacte	618	6	2.2	138	4	Q9NVU8	Q9nvu8 homo sapien
546	6	2.2	126	5	Q9IBH3	Q9ibh3 plasmodium	619	6	2.2	140	12	O65520	O65520 barnah fore
547	6	2.2	126	9	Q9T125	Q9t125 staphylococ	620	6	2.2	141	4	O8TEG2	O8teg2 homo sapien
548	6	2.2	126	10	Q9FZF5	Q9fzf5 arabidopsis	621	6	2.2	141	11	O9DCL1	O9dcl1 mus musculu
549	6	2.2	126	16	Q9KMQ5	Q9kmg5 vibrio chol	622	6	2.2	141	12	O65500	O65500 barnah fore
550	6	2.2	126	16	Q99SQ0	Q99sq0 staphylococ	623	6	2.2	141	12	O65505	O65505 barnah fore
551	6	2.2	126	16	Q97RV8	Q97rv8 streptococ	624	6	2.2	141	12	O65498	O65498 barnah fore
552	6	2.2	126	16	Q9ZLU3	Q9zlu3 helicobacte	625	6	2.2	141	12	O65504	O65504 barnah fore
553	6	2.2	126	16	Q8DQM7	Q8dqm7 streptococ	626	6	2.2	141	12	O65497	O65497 barnah fore
554	6	2.2	127	10	O43202	O43202 triticum ae	627	6	2.2	141	12	O65507	O65507 barnah fore
555	6	2.2	127	10	O42832	O42832 hordeum vul	628	6	2.2	141	12	O65506	O65506 barnah fore
556	6	2.2	127	10	O43303	O43303 glycine max	629	6	2.2	141	12	O65521	O65521 barnah fore
557	6	2.2	127	10	O43203	O43203 triticum ae	630	6	2.2	141	12	O65499	O65499 barnah fore
558	6	2.2	127	10	O42782	O42782 glycine max	631	6	2.2	141	12	O65508	O65508 barnah fore
559	6	2.2	127	10	P94019	P94019 medicago sa	632	6	2.2	141	12	O65516	O65516 barnah fore
560	6	2.2	127	16	O8D4D5	O8d4d5 vibrio vuln	633	6	2.2	141	16	O8DWI3	O8dwi3 streptococ
561	6	2.2	127	17	O27570	O27570 methanobact	634	6	2.2	142	5	O22586	O22586 caenothabdi
562	6	2.2	128	5	Q95W33	Q95w33 haemophilus	635	6	2.2	142	12	O65524	O65524 barnah fore
563	6	2.2	128	11	O8V112	O8v112 rattus norv	636	6	2.2	142	12	O41146	O41146 parametium
564	6	2.2	128	11	Q9DAN8	Q9dan8 mus musculu	637	6	2.2	142	12	O41146	O41146 parametium
565	6	2.2	128	12	O57006	O57006 porcine rep	638	6	2.2	143	2	O9AEW2	O9aew2 pseudomonas
566	6	2.2	128	12	O91H98	O91h98 porcine rep	639	6	2.2	143	5	O9GNF3	O9gnf3 leishmania
567	6	2.2	128	12	O9DH72	O9dh72 porcine rep	640	6	2.2	143	12	O65519	O65519 barnah fore
568	6	2.2	128	12	O91H90	O91h90 porcine rep	641	6	2.2	144	1	O9UW22	O9uw22 sulfobolus
569	6	2.2	128	12	O91HA1	O91ha1 porcine rep	642	6	2.2	144	12	O65522	O65522 barnah fore
570	6	2.2	128	12	O91OG3	O91og3 porcine rep	643	6	2.2	144	12	O83081	O83081 lynchis rin
571	6	2.2	128	12	O91HA3	O91ha3 porcine rep	644	6	2.2	144	17	O8ZVQ5	O8zvg5 pyrobaculum
572	6	2.2	128	12	O91OS5	O91os5 porcine rep	645	6	2.2	146	2	O93P93	O93p93 microscilla
573	6	2.2	128	12	O91H91	O91h91 porcine rep	646	6	2.2	146	2	O33548	O33548 rhodobacter
574	6	2.2	128	12	O8JNL6	O8jnl6 porcine rep	647	6	2.2	146	11	Q9DAB9	Q9dab9 mus musculu
575	6	2.2	128	12	O91H89	O91h89 porcine rep	648	6	2.2	146	12	O65523	O65523 barnah fore
576	6	2.2	128	12	O85023	O85023 porcine rep	649	6	2.2	146	12	O65503	O65503 barnah fore
577	6	2.2	128	12	O57005	O57005 porcine rep	650	6	2.2	146	12	O9EP31	O9ep31 hepatitis c
578	6	2.2	128	12	O91H96	O91h96 porcine rep	651	6	2.2	147	16	O8ETG9	O8etg9 oceanobacil
579	6	2.2	128	12	O91H97	O91h97 porcine rep	652	6	2.2	148	4	O9H1Z8	O9h1z8 homo sapien
580	6	2.2	128	12	O91HA2	O91ha2 porcine rep	653	6	2.2	148	8	O9G8Q7	O9g8q7 naegleria g
581	6	2.2	128	12	O85017	O85017 porcine rep	654	6	2.2	148	16	O65941	O65941 escherichia
582	6	2.2	128	12	O91H99	O91h99 porcine rep	655	6	2.2	148	16	O9KZ19	O9kz19 streptomyc
583	6	2.2	128	12	O9DPB6	O9dpb6 porcine rep	656	6	2.2	149	11	O8BNE8	O8bne8 mus musculu
584	6	2.2	128	12	O9DPB7	O9dpb7 porcine rep	657	6	2.2	149	12	O65518	O65518 barnah fore
585	6	2.2	128	12	O91H95	O91h95 porcine rep	658	6	2.2	150	2	O8KR62	O8kr62 escherichia
586	6	2.2	128	12	O57004	O57004 porcine rep	659	6	2.2	150	16	O9AAK2	O9aak2 caulobacter
587	6	2.2	128	12	O8JNM2	O8jnm2 porcine rep	660	6	2.2	150	16	O981L8	O981l8 rhizobium l
588	6	2.2	128	12	O9WJRO	O9wjro porcine rep	661	6	2.2	150	16	O8G6R4	O8g6r4 bifidobacte
589	6	2.2	128	12	O93162	O93162 porcine rep	662	6	2.2	151	5	P91717	P91717 dugesia tig
590	6	2.2	128	12	O91H86	O91h86 porcine rep	663	6	2.2	152	10	O9FE54	O9fe54 arabidopsis
591	6	2.2	128	12	O55480	O55480 porcine rep	664	6	2.2	152	10	O94E63	O94e63 cryza sativ
592	6	2.2	128	12	O91OG7	O91og7 porcine rep	665	6	2.2	152	16	O8YWH3	O8ywh3 anabaena sp
593	6	2.2	128	12	O91H85	O91h85 porcine rep	666	6	2.2	152	17	O8YWK1	O8ywk1 pyrococcus
594	6	2.2	128	12	O91H93	O91h93 porcine rep	667	6	2.2	153	4	O8N7N1	O8n7n1 homo sapien
595	6	2.2	128	12	O91H94	O91h94 porcine rep	668	6	2.2	153	5	O8WPB1	O8wpb1 toxocara ca
596	6	2.2	128	12	O8BDR9	O8bdr9 porcine rep	669	6	2.2	153	10	O9MAK7	O9mak7 arabidopsis
597	6	2.2	128	12	O8BDR8	O8bdr8 porcine rep	670	6	2.2	153	12	O65501	O65501 barnah fore
598	6	2.2	129	8	O9B8E7	O9b8e7 stylocheiro	671	6	2.2	153	12	O65502	O65502 barnah fore
599	6	2.2	130	5	O9VJ85	O9vj85 drosophila	672	6	2.2	153	12	O65496	O65496 barnah fore
600	6	2.2	130	5	O810N0	O810n0 drosophila	673	6	2.2	153	16	O8EBJ0	O8ebj0 shewanella

674	154	9	080237	080237 bacterioph	747	162	16	032078	032078 bacillus su
675	154	12	091606	091606 hepatitis c	748	163	2	Q9AM04	Q9AM04 staphylococ
676	154	12	091604	091604 hepatitis c	749	163	2	Q9LC46	Q9LC46 staphylococ
677	154	12	091607	091607 hepatitis c	750	163	9	Q8SDJ8	Q8SDJ8 staphylococ
678	154	12	080QV5	080QV5 hepatitis c	751	163	16	Q99SU7	Q99SU7 staphylococ
679	154	12	0816P1	0816P1 hepatitis c	752	163	16	Q8NVR2	Q8NVR2 staphylococ
680	154	12	091603	091603 hepatitis c	753	164	2	Q85988	Q85988 sphingomona
681	154	12	080Q17	080Q17 hepatitis c	754	164	2	O07092	O07092 escherichia
682	154	12	080Q19	080Q19 hepatitis c	755	164	17	Q97BY5	Q97BY5 thermoplasm
683	154	12	080Q19	080Q19 hepatitis c	756	165	2	Q9F8Q1	Q9F8Q1 carboxydoth
684	154	12	091607	091607 hepatitis c	757	165	5	O46217	O46217 drosophila
685	154	12	091603	091603 hepatitis c	758	167	2	Q93338	Q93338 desulfovibr
686	154	12	091607	091607 hepatitis c	759	167	16	Q9KMS2	Q9KMS2 vibrio chol
687	154	12	091606	091606 hepatitis c	760	167	16	Q9KMS2	Q9KMS2 pseudomonas
688	154	12	080Q17	080Q17 hepatitis c	761	168	2	Q85E73	Q85E73 pseudomonas
689	154	12	091607	091607 hepatitis c	762	168	10	Q9C7S3	Q9C7S3 arabisdopsis
690	154	12	091607	091607 hepatitis c	763	168	16	Q9KMS5	Q9KMS5 vibrio chol
691	154	12	091607	091607 hepatitis c	764	168	17	Q9UX13	Q9UX13 sulfobolus
692	154	12	091607	091607 hepatitis c	765	169	16	Q9P9Q4	Q9P9Q4 xylella fas
693	154	12	091607	091607 hepatitis c	766	169	16	Q8ZJ15	Q8ZJ15 yersinia pe
694	154	12	091607	091607 hepatitis c	767	170	2	Q9RGV5	Q9RGV5 salmonella
695	154	12	091607	091607 hepatitis c	768	170	4	O60615	O60615 homo sapien
696	154	12	091607	091607 hepatitis c	769	170	4	Q8IVJ8	Q8IVJ8 homo sapien
697	154	12	080Q14	080Q14 hepatitis c	770	170	10	O22967	O22967 arabisdopsis
698	154	12	080Q14	080Q14 hepatitis c	771	170	10	Q93722	Q93722 pyrobaculum
699	154	12	091607	091607 hepatitis c	772	172	5	Q9GQ62	Q9GQ62 caenorhabdi
700	154	12	091607	091607 hepatitis c	773	172	15	Q99EM2	Q99EM2 human immun
701	154	12	080Q13	080Q13 hepatitis c	774	172	15	Q99EL6	Q99EL6 human immun
702	154	12	091607	091607 hepatitis c	775	172	16	Q98EJ1	Q98EJ1 rhizobium l
703	154	12	091607	091607 hepatitis c	776	172	16	Q8D1F3	Q8D1F3 yersinia pe
704	154	12	091607	091607 hepatitis c	777	172	16	Q8CMX1	Q8CMX1 staphylococ
705	154	12	091607	091607 hepatitis c	778	173	8	Q87662	Q87662 salmonella
706	154	12	091607	091607 hepatitis c	779	173	8	Q8WGE2	Q8WGE2 ranoindes
707	154	12	091607	091607 hepatitis c	780	173	16	Q8XXJ2	Q8XXJ2 ralistonia s
708	154	12	091607	091607 hepatitis c	781	173	16	Q8PMV0	Q8PMV0 corynebacte
709	154	12	091607	091607 hepatitis c	782	174	16	Q8XRW8	Q8XRW8 ralistonia s
710	154	12	091607	091607 hepatitis c	783	175	4	Q9UFY2	Q9UFY2 homo sapien
711	154	12	091607	091607 hepatitis c	784	175	10	Q9LTO7	Q9LTO7 arabisdopsis
712	154	12	091607	091607 hepatitis c	785	176	16	Q8ZRP9	Q8ZRP9 salmonella
713	154	12	091607	091607 hepatitis c	786	177	16	Q92BUB	Q92BUB listeria in
714	154	12	080Q16	080Q16 hepatitis c	787	178	12	Q03729	Q03729 hepatitis c
715	154	12	080Q12	080Q12 hepatitis c	788	178	16	Q8YRT7	Q8YRT7 anabaena sp
716	154	12	091607	091607 hepatitis c	789	179	16	Q8RER4	Q8RER4 fusobacteri
717	154	12	091607	091607 hepatitis c	790	179	16	Q8KGC4	Q8KGC4 chlorobium
718	154	12	091607	091607 hepatitis c	791	180	2	Q9RHL6	Q9RHL6 actinobacil
719	154	12	091607	091607 hepatitis c	792	180	2	O05384	O05384 actinobacil
720	154	12	091607	091607 hepatitis c	793	180	2	O66263	O66263 actinobacil
721	154	12	080Q11	080Q11 hepatitis c	794	180	13	Q09045	Q09045 xenopus lae
722	154	12	091607	091607 hepatitis c	795	180	16	Q8UJ17	Q8UJ17 agrobacteri
723	154	12	091607	091607 hepatitis c	796	181	4	Q8NA89	Q8NA89 homo sapien
724	154	12	091607	091607 hepatitis c	797	181	16	Q97R45	Q97R45 streptococ
725	154	12	091607	091607 hepatitis c	798	181	16	Q8DQ17	Q8DQ17 streptococ
726	154	12	091607	091607 hepatitis c	799	181	17	Q8G306	Q8G306 pyrococcus
727	154	12	091607	091607 hepatitis c	800	182	10	Q9LHU5	Q9LHU5 oryza sativ
728	154	12	091607	091607 hepatitis c	801	182	16	Q8RH71	Q8RH71 fusobacteri
729	154	12	091607	091607 hepatitis c	802	183	8	Q8LX03	Q8LX03 laminaria d
730	154	12	091607	091607 hepatitis c	803	184	8	Q8YJ82	Q8YJ82 brucella me
731	154	12	091607	091607 hepatitis c	804	185	16	Q8RYM0	Q8RYM0 brucella su
732	154	12	091607	091607 hepatitis c	805	186	16	Q86545	Q86545 streptomyce
733	154	12	091607	091607 hepatitis c	806	188	10	Q9C542	Q9C542 arabisdopsis
734	154	12	091607	091607 hepatitis c	807	189	5	O60965	O60965 leishmania
735	154	12	091607	091607 hepatitis c	808	189	15	Q8Q1V4	Q8Q1V4 human immun
736	154	12	091607	091607 hepatitis c	809	189	16	Q9HTG2	Q9HTG2 pseudomonas
737	154	12	091607	091607 hepatitis c	810	189	16	Q98G88	Q98G88 rhizobium l
738	154	12	091607	091607 hepatitis c	811	190	5	Q8ILB0	Q8ILB0 plasmodium
739	154	12	091607	091607 hepatitis c	812	190	11	Q8BSF7	Q8BSF7 mus musculu
740	154	12	091607	091607 hepatitis c	813	190	12	Q83062	Q83062 lettuce mos
741	154	12	091607	091607 hepatitis c	814	191	16	Q9AC28	Q9AC28 caulobacter
742	154	12	091607	091607 hepatitis c	815	191	16	Q8V212	Q8V212 arabisdopsis
743	154	12	091607	091607 hepatitis c	816	193	10	Q8VTH2	Q8VTH2 corynebacte
744	154	12	091607	091607 hepatitis c	817	194	2	O54653	O54653 legionella
745	154	12	091607	091607 hepatitis c	818	194	16	Q97G58	Q97G58 clostridium
746	154	12	091607	091607 hepatitis c	819	195	4	Q8WYLI	Q8WYLI homo sapien

820	6	2.2	195	4	Q96H36	Q96h36 homo sapien	893	218	16	Q8F6E9	Q8f6e9 leptospira
821	6	2.2	195	9	Q9AZM3	Q9azm3 bacterioph	894	219	5	Q8MUT9	Q8mut9 aplysia cal
822	6	2.2	195	9	Q8W740	Q8w740 bacterioph	895	219	5	Q8LQ01	Q8lq01 oryza sativ
823	6	2.2	195	16	Q9C195	Q9c195 lactococcus	896	219	17	Q9YE48	Q9ye48 aeropyrum p
824	6	2.2	195	16	Q8XY18	Q8xy18 ralstonia s	897	219	17	Q8ULX9	Q8ulx9 pyrococcus
825	6	2.2	195	16	Q9RDB2	Q9rdb2 streptomyc	898	220	11	Q8CY73	Q8cy73 mus musculu
826	6	2.2	195	17	Q97W11	Q97w11 sulfolobus	899	220	16	Q8WXY0	Q8wxy0 thermotoga
827	6	2.2	196	9	Q9AZE1	Q9aze1 bacterioph	900	220	16	Q8NSQ0	Q8nsg0 corynebacte
828	6	2.2	196	16	Q9K7G5	Q9k7g5 bacillus ha	901	220	17	Q8HQA1	Q8hqa1 halobacteri
829	6	2.2	196	16	Q9C145	Q9c145 lactococcus	902	221	9	Q8M6Z3	Q8m6z3 cyanophag
830	6	2.2	197	11	Q99LE1	Q99le1 mus musculu	903	221	11	Q99NT6	Q99nt6 cavia lachu
831	6	2.2	198	16	Q98ME5	Q98me5 rhizobium l	904	221	16	Q8F3U8	Q8f3u8 leptospira
832	6	2.2	199	2	Q93F24	Q93f24 pectobacter	905	222	10	Q8Z458	Q8z458 arabidopsis
833	6	2.2	199	16	Q8DCR9	Q8dcr9 vibrio vuln	906	222	16	Q8XM50	Q8xm50 clostridium
834	6	2.2	200	2	Q53660	Q53660 staphylococ	907	223	8	Q8MLN1	Q8mln1 miniotermu
835	6	2.2	200	5	Q8SRF8	Q8srf8 encephalito	908	223	17	Q979V1	Q979v1 thermoplas
836	6	2.2	200	16	Q8ZCY8	Q8zcy8 yersinia pe	909	224	5	Q9TXT5	Q9txt5 caenorhabdi
837	6	2.2	201	2	Q87962	Q87962 streptomyc	910	224	10	Q9FHW4	Q9fhw4 arabidopsis
838	6	2.2	201	10	Q9FEY4	Q9fey4 heterocapsa	911	224	16	Q914Z2	Q914z2 pseudomonas
839	6	2.2	201	16	Q9PQ92	Q9pq92 ureaplasma	912	224	17	Q97B88	Q97b88 thermoplas
840	6	2.2	201	16	Q9KNX6	Q9knx6 vibrio chol	913	225	5	Q9V5R7	Q9v5r7 drosophila
841	6	2.2	201	16	Q8ZE22	Q8ze22 yersinia pe	914	225	5	P91673	P91673 drosophila
842	6	2.2	202	4	Q96F40	Q96f40 homo sapien	915	225	17	Q9HSR5	Q9hsr5 halobacteri
843	6	2.2	202	4	Q96L06	Q96lq6 homo sapien	916	226	5	Q8IU23	Q8iut3 brachiosteo
844	6	2.2	202	8	Q21015	Q21015 choanophal	917	226	8	Q8LYF7	Q8lyf7 chaulioinat
845	6	2.2	202	10	Q949E8	Q949e8 oryza sativ	918	226	16	Q9RRJ9	Q9rrj9 deinococcus
846	6	2.2	202	16	Q8D0L3	Q8d0l3 yersinia pe	919	227	16	Q983J3	Q983j3 rhizobium l
847	6	2.2	203	5	Q95VM3	Q95vm3 nipostrong	920	228	2	P77131	P77131 escherichia
848	6	2.2	203	8	Q21009	Q21009 choanophal	921	228	10	Q94FQ9	Q94fq9 arabidopsis
849	6	2.2	203	16	Q8F6L2	Q8f6l2 leptospira	922	228	10	Q9LYI0	Q9lyi0 arabidopsis
850	6	2.2	204	2	Q8D6L8	Q8d6l8 vibrio vuln	923	228	10	Q8GM01	Q8gm01 oryza sativ
851	6	2.2	204	2	Q9R3D8	Q9r3d8 pseudomonas	924	228	16	Q9RWL7	Q9rw17 deinococcus
852	6	2.2	204	2	Q9R308	Q9r308 pseudomonas	925	228	16	Q8PL44	Q8pl44 xanthomonas
853	6	2.2	204	2	Q9WJ00	Q9wj00 pseudomonas	926	228	16	Q8FK46	Q8fk46 escherichia
854	6	2.2	204	2	Q9R307	Q9r307 pseudomonas	927	229	11	Q91W91	Q91w91 mus musculu
855	6	2.2	204	2	Q9R347	Q9r347 pseudomonas	928	229	12	Q9WHT9	Q9wht9 bluetongue
856	6	2.2	204	2	Q9WJ19	Q9wj19 pseudomonas	929	229	16	Q9AAG0	Q9aag0 caulobacter
857	6	2.2	204	2	Q9RBY4	Q9rby4 pseudomonas	930	229	16	Q97EG6	Q97eg6 clostridium
858	6	2.2	204	2	Q9R3D6	Q9r3d6 pseudomonas	931	229	16	Q8VEJ6	Q8vej6 bruceella me
859	6	2.2	204	2	Q9R436	Q9r436 pseudomonas	932	229	16	Q8G387	Q8g387 bruceella su
860	6	2.2	204	2	Q9R272	Q9r272 pseudomonas	933	229	17	Q9HK08	Q9hk08 thermoplas
861	6	2.2	204	2	Q9R9F3	Q9r9f3 pseudomonas	934	230	5	Q9V5B7	Q9v5b7 drosophila
862	6	2.2	204	2	Q9R3D7	Q9r3d7 pseudomonas	935	230	16	Q8E2V7	Q8e2v7 streptococc
863	6	2.2	206	2	Q9RNL0	Q9rnl0 yzomonas m	936	230	16	Q8DX08	Q8dx08 streptococc
864	6	2.2	206	5	Q95SUL	Q95sul drosophila	937	231	2	Q8KX12	Q8kx12 synechococc
865	6	2.2	206	11	Q9EPQ4	Q9epq4 mus musculu	938	231	12	Q9J968	Q9j968 propouche v
866	6	2.2	206	11	Q8CDE3	Q8cdq3 mus musculu	939	231	16	Q8R7U3	Q8r7u3 thermomae
867	6	2.2	206	16	Q916A6	Q916a6 pseudomonas	940	231	16	Q8F9B1	Q8f9b1 leptospira
868	6	2.2	207	11	Q9QY13	Q9qy13 mus musculu	941	232	5	Q9V5B4	Q9v5b4 drosophila
869	6	2.2	208	5	Q95VX8	Q95vx8 trypanosoma	942	232	11	Q8R345	Q8r345 mus musculu
870	6	2.2	208	11	Q9D3U7	Q9d3u7 mus musculu	943	232	16	Q8DVS9	Q8dvs9 streptococc
871	6	2.2	209	16	Q8NXU9	Q8nxu9 staphylococ	944	233	12	Q98J11	Q98j11 molluscum c
872	6	2.2	210	5	Q8SUF0	Q8suf0 encephalito	945	233	16	Q8YEZ9	Q8yez9 bruceella me
873	6	2.2	211	1	Q977R7	Q977r7 uncultured	946	234	8	Q95F64	Q95f64 eimeria sep
874	6	2.2	211	3	Q9C4R3	Q9c4r3 methanococc	947	234	17	Q9HQX0	Q9hqx0 halobacteri
875	6	2.2	211	3	Q00026	Q00026 ajellomyces	948	235	16	Q92WQ2	Q92wg2 rhizobium m
876	6	2.2	211	4	Q969X0	Q969x0 homo sapien	949	235	10	Q9LR02	Q9lr02 arabidopsis
877	6	2.2	211	16	Q8VKC3	Q8vkc3 mycobacteri	950	236	13	Q9YHW7	Q9yhw7 gallus gall
878	6	2.2	212	5	Q8MPAL	Q8mpal dictyosteli	951	236	17	Q97XZ2	Q97xz2 sulfolobus
879	6	2.2	212	8	Q9T5A5	Q9t5a5 solanum tub	952	238	10	Q8GVJ5	Q8gvj5 oryza sativ
880	6	2.2	213	10	Q948D7	Q948d7 oryza sativ	953	238	11	Q99JR7	Q99jr7 mus musculu
881	6	2.2	213	11	Q9CSB4	Q9csb4 mus musculu	954	238	17	Q95452	Q95452 pyrococcus
882	6	2.2	214	16	Q98SE9	Q98se9 rhizobium l	955	238	17	Q8ZVE9	Q8zve9 pyrobaculum
883	6	2.2	214	17	Q97A59	Q97a59 thermoplas	956	239	4	Q9BPV9	Q9bpv9 homo sapien
884	6	2.2	215	5	Q9ITG9	Q9itg9 biomphalari	957	239	4	Q96SS6	Q96s66 homo sapien
885	6	2.2	215	16	Q92WN5	Q92wn5 rhizobium m	958	239	4	Q9UKD2	Q9ukd2 homo sapien
886	6	2.2	215	16	Q9L0F0	Q9l0f0 streptomyc	959	239	10	Q9FTA2	Q9fta2 arabidopsis
887	6	2.2	216	1	Q9CLR2	Q9clr2 methanococc	960	239	11	Q9D0I8	Q9d0i8 mus musculu
888	6	2.2	216	1	Q9C400	Q9c4q0 methanococc	961	239	11	Q8CS91	Q8cs91 mus musculu
889	6	2.2	216	10	Q94FQ1	Q94fq1 arabidopsis	962	239	16	Q98QJ3	Q98qj3 rhizobium l
890	6	2.2	216	10	Q93WJ3	Q93wj3 arabidopsis	963	239	16	Q92J89	Q92j89 rickettsia
891	6	2.2	216	16	Q98FF4	Q98ff4 rhizobium l	964	240	2	O68993	O68993 chlorobium
892	6	2.2	217	10	Q9LP12	Q9lp12 arabidopsis	965	240	16	Q8G851	Q8g851 bifidobacte

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966 6 2.2 240 16 Q8DP95 Q8dp95 streptococc
967 6 2.2 241 2 P94219 borrellia af
968 6 2.2 241 5 Q8IGD2 Q8igd2 drosophila
969 6 2.2 241 10 Q9LFD2 Q9lf2 arabidopsis
970 6 2.2 241 12 Q84674 Q84674 paramesum
971 6 2.2 241 16 Q8XU43 Q8xu43 ralstonia s
972 6 2.2 242 2 Q9EXK6 Q9exk6 streptomyce
973 6 2.2 242 16 Q9KBR6 Q9kbr6 bacillus ha
974 6 2.2 242 16 Q9CLG8 Q9clg8 pasteurilla
975 6 2.2 242 16 Q8ZKK9 Q8zkk9 salmonella
976 6 2.2 242 16 Q9CEG9 Q9ceg9 lactococcus
977 6 2.2 243 16 Q8K90 Q8k90 rhizobium l
978 6 2.2 243 16 Q8ZM56 Q8zm56 salmonella
979 6 2.2 243 16 Q8PLH4 Q8plh4 xanthomonas
980 6 2.2 244 3 Q06760 Q06760 saccharomyc
981 6 2.2 244 3 Q03888 Q03888 saccharomyc
982 6 2.2 244 10 Q8H8U5 Q8hus5 oryza sativ
983 6 2.2 244 16 Q8Z49 Q8z49 deinococcus
984 6 2.2 244 16 Q99Y06 Q99yd6 streptococc
985 6 2.2 244 16 Q97Q07 Q97q07 streptococc
986 6 2.2 244 16 Q8ZQV6 Q8zqv6 salmonella
987 6 2.2 244 16 Q8Z8D9 Q8z8d9 escherichia
988 6 2.2 244 16 Q8X9C8 Q8x9c8 escherichia
989 6 2.2 244 16 Q8X815 Q8x815 escherichia
990 6 2.2 244 16 Q8ZNN2 Q8znn2 streptococc
991 6 2.2 244 16 Q8K628 Q8k628 streptococc
992 6 2.2 244 16 Q8ZFT5 Q8zft5 versinia pe
993 6 2.2 244 16 Q8FJU6 Q8fju6 oceanobacil
994 6 2.2 244 16 Q8ETD2 Q8etd2 oceanobacil
995 6 2.2 244 16 Q8EAW5 Q8eaw5 shewanella
996 6 2.2 244 16 Q8D5NS Q8d5ns streptococc
997 6 2.2 245 4 Q9NRX8 Q9nrx8 homo sapien
998 6 2.2 245 4 Q9RUT1 Q9rut1 homo sapien
999 6 2.2 245 7 Q31591 Q31591 salmo salar
1000 6 2.2 245 8 Q8MOC9 Q8moc9 amosibidum

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## ALIGNMENTS

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RESULT 1
Q94KL7 ID Q94KL7 PRELIMINARY; PRT; 277 AA.
AC Q94KL7;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Stem secolaricresinol dehydrogenase (Fragment).
OS Forsythia intermedia (Border forsythia).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; Lamiaceae; Oleaceae; Forsythia.
OX NCBI_TaxID=55183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21201084; PubMed=11278426;
RA Xia Z.Q., Costa M.A., Pelissier H.C., Davin L.B., Lewis N.G.;
RT "Seicolaricresinol dehydrogenase Purification, Cloning, and
RT Functional Expression. IMPLICATIONS FOR HUMAN HEALTH PROTECTION."
RL J. Biol. Chem. 276:12614-12623(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF352735; AAK38665.1; --
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
FT NON TER 277
SQ SEQUENCE 277 AA; 29256 MW; 98885C210CAFE2EB CRC64;

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Query Match 40.3%; Score 110; DB 10; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-110;

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Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ARLEGKVALITGGASGIGETTAKLFSQHGAIAIADVQDELGHSVVEAIGTSNYSYIHC 67
Db 12 ARLEGKVALITGGASGIGETTAKLFSQHGAIAIADVQDELGHSVVEAIGTSNYSYIHC 71
Qy 68 DVTNEDGVKNADVNTVSTYGLKIMFNSNAGISDPNRRPRIIDNEKADPERV 117
Db 72 DVTNEDGVKNADVNTVSTYGLKIMFNSNAGISDPNRRPRIIDNEKADPERV 121

RESULT 2
Q40590 ID Q40590 PRELIMINARY; PRT; 234 AA.
AC Q40590;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE THP-1 protein.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; Lamiaceae; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Petite Havana SR-1;
RX MEDLINE=95004656; PubMed=7920706;
RA Kawaoka A., Kawamoto T., Sekine M., Yoshida K., Takano M., Shinmyo A.;
RT "A cis-acting element and a trans-acting factor involved in the wound-
RT induced expression of a horsetadish peroxidase gene.";
RL Plant J. 6:87-97(1994).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; D29976; BAA06241.1; --
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
KW Oxidoreductase.
SQ SEQUENCE 234 AA; 25078 MW; F10BD4E0FF97940A CRC64;

```

Query Match 6.2%; Score 17; DB 10; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 10 RLEGKVALITGGASGIG 26
Db 13 RLEGKVALITGGASGIG 29

RESULT 3
O50038 ID O50038 PRELIMINARY; PRT; 284 AA.
AC O50038;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Short chain alcohol dehydrogenase.
GN SCANT.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; Lamiaceae; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Moenke G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=96145513; PubMed=8555446;
RA Herbers K., Moenke G., Badur R., Sonnenwald U.;

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Query Match 40.3%; Score 110; DB 10; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-110;

RT "A simplified procedure for the subtractive cDNA cloning of  
RT photoassimilate-responding genes: isolation of cDNAs encoding a new  
RT class of pathogenesis-related proteins."  
CC Plant Mol. Biol. 29:1027-1038(1995).

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.

DR EMBL; AJ223178; CAA11154.1; -.  
DR EMBL; AJ223177; CAA11153.1; -.  
DR HSSP; P19992; IHDC.  
DR InterPro; IPR002198; ADH short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 284 AA; 29819 MW; BD884E9013FB63E9 CRC64;

Query Match 6.2%; Score 17; DB 10; Length 284;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RLEGKVALITGASGIG 26  
Db 13 RLEGKVALITGASGIG 29

RESULT 4

Q9ZR17 ID Q9ZR17 PRELIMINARY; PRT; 283 AA.

AC Q9ZR17; AC Q9ZR17;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Putative alcohol dehydrogenase.

GN F4C21.6 OR At4G03140.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K.,

RA Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,

RA McCombie W.R.;

RT "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cm.;"

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,

RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,

RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,

RA Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

DR EMBL; AC005275; AAD14442.1; -.

DR EMBL; AL161496; CAB7799.1; -.

DR HSSP; P19992; IHDC.

DR InterPro; IPR002198; ADH short.

DR Pfam; PF00106; adh\_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH\_SHORT; 1.

KW Oxidoreductase.

SQ SEQUENCE 283 AA; 29994 MW; 93B0A97CECC859BC CRC64;

Query Match 5.9%; Score 16; DB 10; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGASGIG 26  
Db 18 LEGKVALITGASGIG 33

RESULT 5

Q941E4 ID Q941E4 PRELIMINARY; PRT; 306 AA.

AC Q941E4; AC Q941E4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE AT3g26770/MDJ14\_21.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayaeshizaki Y.,

RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

RA Ecker J.R.;

RT "Arabidopsis cDNA clones.;"

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

DR EMBL; AY052216; AAK97686.1; -.

DR InterPro; IPR002198; ADH\_short.

DR Pfam; PF00106; adh\_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

KW Oxidoreductase.

SQ SEQUENCE 306 AA; 31795 MW; C1816892BF71B537 CRC64;

Query Match 5.1%; Score 14; DB 10; Length 306;

Best Local Similarity 100.0%; Pred. No. 3.2e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGASG 24

Db 41 LEGKVALITGASG 54

RESULT 6

Q9LW34 ID Q9LW34 PRELIMINARY; PRT; 306 AA.

AC Q9LW34; AC Q9LW34;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Alcohol dehydrogenase-like protein (At3g26770/MDJ14\_21).

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC

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RT clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan V.W., Iehida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Mikanda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL "Arabidopsis ORF clones.";
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AB016889; BA001223.1; -.
DR EMBL; AY143855; AA28794.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 306 AA; 31783 MW; 8E87A72D081266EB CRC64;

Query Match
Best Local Similarity 5.1%; Score 14; DB 10; Length 306;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LEGKVALITGGASG 24
Db 41 LEGKVALITGGASG 54

RESULT 7
P93697 ID P93697 PRELIMINARY; PRT; 267 AA.
AC P93697
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE CprD12 protein.
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Ehretidae; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3917;
RN [1]
RP SEQUENCE FROM N.A.
RA Ichi S., Yamaguchi, Shinozaki K., Urao T., Shinozaki K.;
RT "Characterization of two cDNAs for novel drought-inducible genes in
RT the high drought-tolerant cowpea.";
RL J. Plant Physiol. Res. 109:415-424(1996).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; D88121; BA13541.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 267 AA; 28484 MW; 8C4A48A2B9F41B64 CRC64;

Query Match
Best Local Similarity 4.8%; Score 13; DB 10; Length 267;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AVELGQFGIRVNC 189
Db 178 AVELGQFGIRVNC 190

us-09-673-918a-2.oligo.rspt

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RESULT 8
O8H0D9 ID O8H0D9 PRELIMINARY; PRT; 274 AA.
AC O8H0D9
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adh1onol dehydroge.
OS Phaseolus lunatus (Lima bean) (Phaseolus limensis).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Viciales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3884;
RN [1]
RP SEQUENCE FROM N.A.
RA Koriuchi J., Arimura G., Ozawa R., Muroi A., Takabayashi J.,
RA Nishiohara T.,
RT "Phaseolus lunatus ";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086038; BAC53872.1; -.
SQ SEQUENCE 274 AA; 28662 MW; DEC858BDB324877F CRC64;

Query Match
Best Local Similarity 4.8%; Score 13; DB 10; Length 274;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AVELGQFGIRVNC 189
Db 178 AVELGQFGIRVNC 190

RESULT 9
O8LID4 ID O8LID4 PRELIMINARY; PRT; 321 AA.
AC O8LID4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OJ1343.D04.14 protein (P0453E03.33 protein).
GN OJ1343.D04.14 OR P0453E03.33.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OJ1343.D04.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0453E03.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AP003825; BAC10093.1; -.
DR EMBL; AP005452; BAC22441.1; -.
DR Gramene; O8LID4; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 321 AA; 34337 MW; 3DB5EC4726D98AA2 CRC64;

Query Match
Best Local Similarity 4.8%; Score 13; DB 10; Length 321;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RC	STRAIN=H/7-2;		
PA	Tsuchiya T	Suwahe K	Watake T
			Kosawa Y
			Kosawa Y

```

OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT 'S'-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072447; AAC35340.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
SQ SEQUENCE 284 AA; 29898 MW; 2B54BFFBAD6BAE4A CRC64;

Query Match 4.4%; Score 12; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97
Db 89 YGKLDIMFSNAG 100

RESULT 14
O82465 PRELIMINARY; PRT; 284 AA.
AC O82465;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Short-chain alcohol dehydrogenase.
DS SP.
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT 'S'-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072447; AAC35340.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
SQ SEQUENCE 284 AA; 29823 MW; 4C04A888178C0633 CRC64;

Query Match 4.4%; Score 12; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97
Db 89 YGKLDIMFSNAG 100

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RESULT 15
P87017 PRELIMINARY; PRT; 278 AA.
ID P87017;
AC P87017;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Short-chain alcohol dehydrogenase.
DS ADHA.
OS Aspergillus parasiticus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic trichocomaceae; Aspergillus.
OX NCBI_TaxID=5067;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang P.K., Yu J., Ehrlich K.C., Boue S.M., Montalbano B.G.,
RA Bhatnagar D., Cleveland T.E.;
RT "adha in Aspergillus parasiticus Is Involved in Conversion of 5'-
RT Hydroxyaverrantin to Averufin.";
RL Appl. Environ. Microbiol. 66:4715-4719(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; U76621; AAB51228.3; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PS00061; ADH_SHORT; 1.
DR Oxidoreductase.
SQ SEQUENCE 278 AA; 29557 MW; 8C60C5437EB9B871 CRC64;

Query Match 4.0%; Score 11; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ALITGGASGIG 26
Db 18 ALITGGASGIG 28

Search completed: October 23, 2003, 13:05:29
Job time : 163 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2003, 12:37:54 ; Search time 85 Seconds  
(without alignments)  
509.792 Million cell upd

**Title:** US-09-673-918A-2

Perfect score:

Sequence: 1 MQLRTAFARRLEGKVALITG.....IDGGFSVCNSVIKVFOYPDS 273

Scoring table: BLOSUM62

Scoring card: 200002  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs. 158726573 residues

Total number of bits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 45 summaries

Database : A Geneset 19-Jun-03.\*

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22: /SIDSI/cgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/cgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/cgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1393	100.0	273	21	RAY54412
2	1388	99.6	272	21	RAY54420
3	1364	97.9	277	21	RAY54413
4	1233	88.5	276	21	RAY54416
5	1233	88.5	276	23	AAO21494
6	1223	87.8	273	21	RAY54414
7	1175	84.4	277	21	RAY54415
8	658.5	47.3	285	23	ABB91329
9	654.5	47.0	285	21	AAG35524

## ALIGNMENTS

RESULT 1  
AAY54412

AA154412  
ID AAY54412 standard: Protein: 273 AA.

XX  
AC  
BAY54A12.

XX

DT 06-APR-2000 (first entry)

DE Secoisolaricresinol dehydrogenase protein clone DEHY133.

KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;

enterolactone: enterodiol: dietary supplement: enterolactone; heart-protecting agent; phytoestrogen, lignan; matairesinol; heart-protecting agent

KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

OS Forsythia intermedia.

PN WO9955846-A1.

04-NOV-1999

XX  
DE 22-7555-1000.  
99WC-11509075

XX

XX

**XX**

XX  
FI  
IVIA 2, COSTA RM, D

DR WPI; 2000-126356/  
N-PCDB: A2745730

XX

PT New nucleic acid molecule encoding an enzyme involved in lignan  
 BT biosynthetic pathway, useful for producing large amounts of lignans  
 XX Claim 8; Page 46-47; 66pp; English.  
 XX  
 CC The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX Sequence 273 AA;  
 SQ  
 Query Match 100.0%; Score 1393; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-130;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS 60  
 DB 1 MQLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS 60  
 QY 61 NSTYIHCDVTNEDGVKNAVDNTVSTYTKLDMFNSNAGISDPNRPRIIDNEKADFERVLSV 120  
 DB 61 NSTYIHCDVTNEDGVKNAVDNTVSTYTKLDMFNSNAGISDPNRPRIIDNEKADFERVLSV 120  
 QY 121 NVTVGFLCMKHAARVMI PARSGNIISTASLSSTMTGGSSHAYCGSKHAVLALTRNLAVEL 180  
 DB 121 NVTVGFLCMKHAARVMI PARSGNIISTASLSSTMTGGSSHAYCGSKHAVLALTRNLAVEL 180  
 QY 181 GQFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNLKGPKNVEDVANAALYLA 240  
 DB 181 GQFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNLKGPKNVEDVANAALYLA 240  
 QY 241 SDEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 273  
 DB 241 SDEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 273  
 RESULT 2  
 AAY54420  
 ID AAY54420 standard; Protein; 272 AA.  
 XX AC AAY54420;  
 XX DT 06-APR-2000 (first entry)  
 XX DE Secoisolariciresinol dehydrogenase protein clone DEHV130.  
 KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; nutraceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX Forsythia intermedia.  
 XX WO9955846-A1.  
 XX

PD 04-NOV-1999.  
 XX 23-APR-1999; 99WO-US08975.  
 XX 24-APR-1998; 98US-0082977.  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX Xia Z, Costa MA, Davin LB, Lewis NG;  
 WPI; 2000-126356/11.  
 N-ESDB; AAZ45743.  
 PT New nucleic acid molecule encoding an enzyme involved in lignan  
 BT biosynthetic pathway, useful for producing large amounts of lignans  
 XX Example 2; Page 61-63; 66pp; English.  
 CC The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX Sequence 272 AA;  
 SQ  
 Query Match 99.6%; Score 1388; DB 21; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-110;  
 Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 61  
 DB 1 QLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 60  
 QY 62 STYIHCDVTNEDGVKNAVDNTVSTYTKLDMFNSNAGISDPNRPRIIDNEKADFERVLSV 121  
 DB 61 STYIHCDVTNEDGVKNAVDNTVSTYTKLDMFNSNAGISDPNRPRIIDNEKADFERVLSV 120  
 QY 122 VTGVFLCMKHAARVMI PARSGNIISTASLSSTMTGGSSHAYCGSKHAVLALTRNLAVELG 181  
 DB 121 VTGVFLCMKHAARVMI PARSGNIISTASLSSTMTGGSSHAYCGSKHAVLALTRNLAVELG 180  
 QY 182 QFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNLKGPKNVEDVANAALYLA 241  
 DB 181 QFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNLKGPKNVEDVANAALYLA 240  
 QY 242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 273  
 DB 241 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 272  
 RESULT 3  
 AAY54413  
 ID AAY54413 standard; Protein; 277 AA.  
 XX AC AAY54413;  
 XX

```

DT 06-APR-2000 (first entry)
DE Secoisolariciresinol dehydrogenase protein clone SMDBHY321.
XX
XX Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;
KW lignan; matairesinol; health-protecting lignan; phytoestrogen;
KW enterolactone; enterodiol; neutriceutical; dietary supplement;
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
XX
OS Forsythia intermedia.
XX
XX WO9955846-A1.
XX
XX 04-NOV-1999.
XX
XX 23-APR-1999; 99WO-US08975.
XX
XX 24-APR-1998; 98US-0082977.
XX
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
XX Xia Z, Costa MA, Davin LB, Lewis NG;
XX WPI; 2000-126356/11.
XX DR N-PSDB; AAZ45731.
XX
XX New nucleic acid molecule encoding an enzyme involved in lignan
XX biosynthetic pathway, useful for producing large amounts of lignans -
XX
XX Claim 8; Page 49-50; 66pp; English.
XX
XX The present sequence represents a secoisolariciresinol dehydrogenase
XX protein. The enzyme is involved in the lignan biosynthetic pathway.
XX The secoisolariciresinol dehydrogenase proteins have a molecular
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require
XX NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase
XX nucleic acids are used for the recombinant expression of the enzymes.
XX It is also used to obtain expression or enhanced expression of
XX secoisolariciresinol dehydrogenase in plants or to alter lignan
XX biosynthesis. The enzyme is used for production of the pharmacologically
XX active lignan, matairesinol. The secoisolariciresinol dehydrogenase
XX proteins and nucleic acids can be utilized to: elevate or otherwise
XX alter the levels of health-protecting lignans, including phytoestrogens
XX such as enterolactone and enterodiol, in plant species, including
XX vegetables, grains and fruits and to food items incorporating material
XX derived from such genetically altered plants; genetically alter plant
XX species to provide an abundant, natural supply of lignans useful for
XX a variety of purposes, for example as neutriceuticals and dietary
XX supplements; to genetically alter living organisms to produce an
XX abundant supply of optically pure lignans having desirable biological
XX properties, for example (-)-trachelogenin which possesses antiviral
XX properties, and (-)-podophyllotoxin.
XX
XX SQ Sequence 277 AA;
XX
XX Query Match 97.9%; Score 1364; DB 21; Length 277;
XX Best Local Similarity 98.2%; Pred. No. 1.8e-127;
XX Matches 267; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX 2 QLRFAARRLEGGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSWBEAIGTSN 61
XX : |||||
XX 6 QVLTAAARRLEGGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSWBEAIGTSN 65
XX : |||||
XX
XX 62 STYIHCVDVTNEDGVKNVAVNTVSTYTGKLDINFNSNAGISDPNRIIDNEKADFERVLSVN 121
XX : |||||
XX 66 STYIHCVDVTNEDGVKNVAVNTVSTYTGKLDINFNSNAGISDPNRIIDNEKADFERVFSVN 125
XX : |||||
XX
XX 122 VTGFLCMKHAAKVMIPARSGNIISTASLSMTGSGSHAYCGSKHVALTRNLAVELG 181
XX : |||||
XX 126 VTGFLCMKHAAKVMIPARSGNIISTASLSMTGSGSHAYCGSKHVALTRNLAVELG 185
XX : |||||
XX 182 QFGRVNCNLSPPFGLPTALGKKFSGIKNEEFENVINPAGNLKGPKNVEDVANALYLAS 241
XX : |||||
XX
XX Db 186 QFGRVNCNLSPPFGLPTALGKKFSGIKNEEFENVINPAGNLKGPKNVEDVANALYLAS 245
XX
XX Qy 242 DEAKYVSGHNLFDIDGGFSVCNVIKVFQYPDS 273
XX : |||||
XX Db 246 DEAKYVSGHNLFDIDGGFSVCNVIKVFQYPDS 277
XX : |||||
XX
XX RESULT 4
XX AAY54416
XX ID AAY54416 standard; Protein; 276 AA.
XX
XX AC AAY54416;
XX
XX XX 06-APR-2000 (first entry)
XX
XX XX Secoisolariciresinol dehydrogenase protein clone SMDBHY631.
XX
XX XX Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;
KW lignan; matairesinol; health-protecting lignan; phytoestrogen;
KW enterolactone; enterodiol; neutriceutical; dietary supplement;
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
XX
XX XX Forsythia intermedia.
XX
XX XX WO9955846-A1.
XX
XX XX 04-NOV-1999.
XX
XX XX 23-APR-1999; 99WO-US08975.
XX
XX XX 24-APR-1998; 98US-0082977.
XX
XX XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
XX XX Xia Z, Costa MA, Davin LB, Lewis NG;
XX WPI; 2000-126356/11.
XX DR N-PSDB; AAZ45734.
XX
XX New nucleic acid molecule encoding an enzyme involved in lignan
XX biosynthetic pathway, useful for producing large amounts of lignans -
XX
XX Claim 8; Page 56-57; 66pp; English.
XX
XX The present sequence represents a secoisolariciresinol dehydrogenase
XX protein. The enzyme is involved in the lignan biosynthetic pathway.
XX The secoisolariciresinol dehydrogenase proteins have a molecular
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require
XX NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase
XX nucleic acids are used for the recombinant expression of the enzymes.
XX It is also used to obtain expression or enhanced expression of
XX secoisolariciresinol dehydrogenase in plants or to alter lignan
XX biosynthesis. The enzyme is used for production of the pharmacologically
XX active lignan, matairesinol. The secoisolariciresinol dehydrogenase
XX proteins and nucleic acids can be utilized to: elevate or otherwise
XX alter the levels of health-protecting lignans, including phytoestrogens
XX such as enterolactone and enterodiol, in plant species, including
XX vegetables, grains and fruits and to food items incorporating material
XX derived from such genetically altered plants; genetically alter plant
XX species to provide an abundant, natural supply of lignans useful for
XX a variety of purposes, for example as neutriceuticals and dietary
XX supplements; to genetically alter living organisms to produce an
XX abundant supply of optically pure lignans having desirable biological
XX properties, for example (-)-trachelogenin which possesses antiviral
XX properties, and (-)-podophyllotoxin.
XX
XX SQ Sequence 276 AA;
XX
XX Query Match 88.5%; Score 1233; DB 21; Length 276;
XX Best Local Similarity 88.2%; Pred. No. 2.1e-114;
XX Matches 240; Conservative 14; Mismatches 18; Indels 0; Gaps 0;
XX
XX 2 QLRFAARRLEGGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSWBEAIGTSN 61
XX : |||||

```

Db 5 QLTAFARLEGGKVALITGASGVGEVTAKLPSQHGAKVAIADVODELGHVSVEAIGLSN 64  
 QY 62 STYIHCDVTNEDGVKNVANDTSTYTGKLDIMFNSNAGISDPNRPRIIDNEKADFERVLSVN 121  
 Db 65 STYIHCDVTNEDGVKNVANDTSTYTGKLDIMFNNAGISDPYKPRVIDNEKADFERVLSVN 124  
 QY 122 VTGVFLCMKHAARVIMPARSGNIIISTASLSSTMGSGSHAYCGSKHVAVLALTRNLAVELG 181  
 Db 125 VTGVFLCMKHAARVIMPARSGCIIISTASLSSTMGSGSHAYCGSKHVAVLGLTRNLAVELG 184  
 QY 182 QFGIRVNCNLSPPFGLPTALCKFKSGIKNEEPEENVINFAGNLKGPKFNVEDVANAALYLAS 241  
 Db 185 QFGIRVNCNLSPPFGLPTPLAKKFTGIENDEDLANGIERAGNLKGTGLRIEDVANAALFLAS 244  
 QY 242 DEAKYVSGHNLFDGGFVSCNVIKVOYQPD 273  
 Db 245 DEAQYVSGQNLFDGGFVSCNVAIKLFQYDPS 276  
 RESULT 5  
 AAO21494  
 ID AAO21494 standard; Protein; 276 AA.  
 AC AAO21494;  
 XX  
 DT 15-AUG-2002 (first entry)  
 DE Secoisolariciresinol dehydrogenase protein.  
 DE Guaiacyl (G)-lignan; monocotyledon plant; rice; food additive;  
 KW seed-specific transcriptional regulatory region; dehydrogenase; enzyme.  
 KW Unidentified.  
 OS  
 XX WO200220548-A1.  
 XX 14-MAR-2002.  
 XX  
 XX 04-SEP-2001; 2001WO-US27500.  
 XX  
 XX 07-SEP-2000; 2000US-230632P.  
 XX  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PA (PHYT-) APPLIED PHYTOLOGICS INC.  
 XX  
 XX Lewis NG, Davin LB, Huang N;  
 DR WPI; 2002-425767/45.  
 DR N-PSDB; AAL38432.  
 XX  
 XX Increasing guaiacyl-lignan content in monocotyledon plants, by  
 FT transforming plant with chimeric gene construct having seed-specific  
 FT transcriptional regulator linked to gene encoding protein involved in  
 FT G-lignan formation  
 XX  
 XX Claim 2; Fig 10; 136pp; English.  
 XX  
 XX The invention relates to a method for increasing the guaiacyl (G)-lignan  
 CC content in seeds of a monocotyledon plant, comprising selecting at least  
 CC one protein or enzyme integral to the pathway leading to G-lignan  
 CC formation, stably transforming a monocotyledon plant with chimeric gene  
 CC (CG) constructs having a seed-specific transcriptional regulatory region  
 CC operably linked to a nucleic acid sequence encoding the enzyme. The  
 CC method of the invention is useful for stably transforming a  
 CC monocotyledonous plant (e.g. rice) with CG constructs resulting in  
 CC increased expression of the genes encoded by CG constructs. The G-lignan  
 CC enriched seed composition is useful as a food additive. This  
 CC sequence represents the secoisolariciresinol dehydrogenase protein  
 CC relating to the invention.  
 XX  
 XX Sequence 276 AA;  
 SQ

Query Match 88.5%; Score 1233; DB 23; Length 276;  
 Best Local Similarity 88.2%; Pred. No. 2.1e-114; Indels 0; Gaps 0;  
 Matches 240; Conservative 14; Mismatches 18;  
 QY 2 QLTAFARLEGGKVALITGASGIGETTAKLPSQHGAKVAIADVODELGHVSVEAIGTSN 61  
 Db 5 QLTAFARLEGGKVALITGASGVGEVTAKLPSQHGAKVAIADVODELGHVSVEAIGLSN 64  
 QY 62 STYIHCDVTNEDGVKNVANDTSTYTGKLDIMFNSNAGISDPNRPRIIDNEKADFERVLSVN 121  
 Db 65 STYIHCDVTNEDGVKNVANDTSTYTGKLDIMFNNAGISDPYKPRVIDNEKADFERVLSVN 124  
 QY 122 VTGVFLCMKHAARVIMPARSGNIIISTASLSSTMGSGSHAYCGSKHVAVLALTRNLAVELG 181  
 Db 125 VTGVFLCMKHAARVIMPARSGCIIISTASLSSTMGSGSHAYCGSKHVAVLGLTRNLAVELG 184  
 QY 182 QFGIRVNCNLSPPFGLPTALCKFKSGIKNEEPEENVINFAGNLKGPKFNVEDVANAALYLAS 241  
 Db 185 QFGIRVNCNLSPPFGLPTPLAKKFTGIENDEDLANGIERAGNLKGTGLRIEDVANAALFLAS 244  
 QY 242 DEAKYVSGHNLFDGGFVSCNVIKVOYQPD 273  
 Db 245 DEAQYVSGQNLFDGGFVSCNVAIKLFQYDPS 276  
 RESULT 6  
 AAY54414  
 ID AAY54414 standard; Protein; 273 AA.  
 AC AAY54414;  
 XX  
 DT 06-APR-2000 (first entry)  
 DE Secoisolariciresinol dehydrogenase protein clone SMDEHY431.  
 DE Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; metairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX Forsythia intermedia.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 120 /note= "encoded by GTN"  
 FT Misc-difference 122 /note= "encoded by GTN"  
 FT  
 XX WO9955846-A1.  
 XX  
 XX 04-NOV-1999.  
 XX  
 XX 23-APR-1999; 99WO-US08975.  
 XX  
 XX 24-APR-1998; 98US-0082977.  
 XX  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX  
 XX Xia Z, Costa MA, Davin LB, Lewis NG;  
 XX WPI; 2000-126356/11.  
 XX N-PSDB; AAZ45732.  
 XX  
 XX New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans  
 XX  
 XX Claim 8; Page 51-52; 66pp; English.  
 XX  
 XX The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase

CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 273 AA;  
 Query Match 87.8%; Score 1223; DB 21; Length 273;  
 Best Local Similarity 86.8%; Pred. No. 2e-113;  
 Matches 237; Conservative 15; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 MQLRTAFARRLEGGKVALITGGASGIGETAKLFSQHGAQVAIADVQDELGHSHVVEAIGTS 60  
 Db 1 MQLRTAIAARRLEGGKVALITGGASGIGETAKLFSQHGAQVAIADVQDELGHSHVVEAIGTS 60  
 Qy 61 NSTYHCDVTNEDGVKNADVNTVSTYGLDIFMSNAGISDPNRPRIIDNEKADFERVLVS 120  
 Db 61 NSTYHCDVTNEDGVKNADVNTVSTYGLDIFMSNAGISDPYKPRVIDNEKADFERVLVSX 120  
 Qy 121 NVTGFLCMKHAARVMIPARSGNIISTASLSTWGGSSSHAYCGSKHVALALTRNLAVEL 180  
 Db 121 NKTGVFLPMKHAARIMVPAFGNCIIISTASLSTWGGSSSHAYCGKHAVALGLTRNLAVEL 180  
 Qy 181 QGFGIRVNCNLSPPFGLPTALGKFKSGIKNEEBFENVINPAGNLKGFKNVEDVANAALYLA 240  
 Db 181 QGFGIRVNCNLSPPFGLPTALGKFKSGIENDVDFAAIEHAGNLKGTGLRIEDVANAALFLA 240  
 Qy 241 SDEAKYVSGHNLFDIDGFSVCNSVTKVFPYDPS 273  
 Db 241 SDEAKYVSGQNLFDIDGFSVCNSAIKMFQYDPS 273  
 RESULT 7  
 AAY54415  
 ID AAY54415 standard; Protein; 277 AA.  
 XX  
 AC AAY54415;  
 XX  
 DT 06-APR-2000 (first entry)  
 XX  
 DE Secoisolariciresinol dehydrogenase protein clone SMDEHY511.  
 XX  
 KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; nutraceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX  
 OS Forsythia intermedia.  
 XX  
 FN WO9955846-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 23-APR-1999; 98WO-US089975.  
 XX  
 PR 24-APR-1998; 98US-0082977.  
 XX  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX  
 FI Xia Z, Costa MA, Davin LB, Lewis NG;  
 XX

DR WPI; 2000-126356/11.  
 XX N-PSDB; AAZ45733.  
 PT New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans -  
 PS Claim 8; Page 54-55; 66pp; English.  
 XX  
 CC The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 277 AA;  
 Query Match 84.4%; Score 1175; DB 21; Length 277;  
 Best Local Similarity 83.5%; Pred. No. 1.3e-108;  
 Matches 227; Conservative 20; Mismatches 25; Indels 0; Gaps 0;  
 Qy 2 QLRTAFARRLEGGKVALITGGASGIGETAKLFSQHGAQVAIADVQDELGHSHVVEAIGTSN 61  
 Db 6 QVLTAIRTRLEGGKVALITGGASGIGETAKLFSQHGAQVAIADVQDELGHSHVVEAIGTSN 65  
 Qy 62 STYHCDVTNEDGVKNADVNTVSTYGLDIFMSNAGISDPNRPRIIDNEKADFERVLVS 121  
 Db 66 SIXHCDVTNEDDVKNAADVNTVSTYGLDIFMNFAGIADPNKPRIVDNEKADFERVLVS 125  
 Qy 122 VTGFLCMKHAARVMIPARSGNIISTASLSTWGGSSSHAYCGSKHVALALTRNLAVELG 181  
 Db 126 VTGFLCMKHAARVMVPAFGNCIIISTASVSTTGGAAASHAYCCSKHVALGLTRNLAVELG 185  
 Qy 182 QFGIRVNCNLSPPFGLPTALGKFKSGIKNEEBFENVINPAGNLKGFKNVEDVANAALYLA 241  
 Db 186 QFGIRVNCNLSPPFGLPTALGKFKSVLENDDELENAMSLMGNLKGTLNKAEDVANAALYLA 245  
 Qy 242 DEAKYVSGHNLFDIDGFSVCNSVTKVFPYDPS 273  
 Db 246 DEAKYVSGHNLFDIDGFSVTSNAIKMFQYDPT 277  
 RESULT 8  
 ABB91329  
 ID ABB91329 standard; Protein; 285 AA.  
 XX  
 AC ABB91329;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 540.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FN WO200210210-A2.  
 XX



PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160788.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-0147303.			
PR	06-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-0147493.			
PR	09-AUG-1999;	99US-0147935.			
PR	10-AUG-1999;	99US-0148171.			
PR	11-AUG-1999;	99US-0148319.			
PR	12-AUG-1999;	99US-0148341.			
PR	13-AUG-1999;	99US-0148565.			
PR	13-AUG-1999;	99US-0148684.			
PR	16-AUG-1999;	99US-0149368.			
PR	17-AUG-1999;	99US-0149175.			
PR	18-AUG-1999;	99US-0149426.			
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
PR	27-AUG-1999;	99US-0151080.			
PR	30-AUG-1999;	99US-0151303.			
PR	31-AUG-1999;	99US-0151438.			
PR	01-SEP-1999;	99US-0151930.			
PR	07-SEP-1999;	99US-0152363.			
PR	10-SEP-1999;	99US-0153070.			
PR	13-SEP-1999;	99US-0153758.			
PR	15-SEP-1999;	99US-0154018.			
PR	16-SEP-1999;	99US-0154039.			
PR	20-SEP-1999;	99US-0154779.			
Query Match					
47.0%; Score 654.5; DB 21; Length 285;					
Best Local Similarity 50.9%; Pred. No. 1.1e-56;					
Matches 139; Conservative 42; Mismatches 79; Indels 13; Gaps 5;					
Qy	8	ARRLEGVALITGASGIGETTAKLFSOHGAKVAIADVDLGHVSVEAI--GTSNST--	63		
Db	15	SQRLGKVALITGGATGIGESIVLPHKHKAKVICVLQDDLGGEVCKSLRGESKETAF	74		
Qy	64	YIHCDVTNEDGVKNAVDNTVSTYGLDIMFSNAGISDPNRPRIIDNEKADPERVLSVNV	123		
Db	75	PIHGDVREDDISNAVDFAVKNFOTLDLILNAGLCGAPCPDIRNYSILSEFEMTFDNNV	134		
Qy	124	GVFLCMKHAARVMIIPARSGNIISTASLSSTWTGGSSHAYCGSKHAVIALTRNLAVEL	183		
Db	135	GAFLSMKHAARVMIPEKKGSIVSLCSVGVGVGPHSVYVGSKHAVLGLTRSVAAELQ	194		
Qy	184	GIRVNCCLSPCLPTALCKKFSGINKNEEFENVI----NFA---GNLKGPKNFVEDVANA	236		
Db	195	GIRVNCVSPXAVATKLA--LAHLPEERTEDAFVGFRNFAAANANLKGVELTVGDVAN	252		
Qy	237	LYLASDEAKVYSGHNLFIDGGFSVCNSVIKVFQ	269		
Db	253	LFLASDDSRVYISGDNLMIDGGFTCTNHSFKVFR	285		
RESULT 10					
ABB92624					
ID	ABB92624 standard; Protein; 303 AA.				
XX	ABB92624;				
AC	ABB92624;				
XX	31-MAY-2002 (first entry)				
DT					
XX					

DE Herbicidally active polypeptide SEQ ID NO 1835.  
 XX Herbicidal; plant; agriculture; herbicide.  
 KW Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 PN WO200210210-A2.  
 XX 07-FEB-2002.  
 XX 28-AUG-2001; 2001WO-EP09892.  
 XX 28-AUG-2001; 2001WO-EP09892.  
 XX (FARB ) BAYER AG.  
 XX Tietjen K, Weidler M;  
 XX WPI; 2002-269010/31.  
 XX Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms  
 XX Claim 5; SEQ ID NO 1835; 261pp + Sequence Listing; English.  
 XX The invention relates to identifying target proteins  
 CC (AB590790-AB594016) for herbicidally active compounds, comprising  
 CC aligning and comparing nucleic acid or amino acid sequences from plant  
 CC with nucleic acid or amino acid sequences from non-plant organisms using  
 CC suitable search parameters, where plant sequences having an E-value  
 CC greater by a factor of 3 than the E-value of most similar non-plant  
 CC sequences are selected. The polypeptides or nucleic acids encoding them  
 CC are useful for identifying modulators. The identified modulators are  
 CC useful as herbicides.  
 XX SQ Sequence 303 AA;  
 Query Match 44.9%; Score 625.5; DB 23; Length 303;  
 Best Local Similarity 47.5%; Pred. No. 9,4e-54;  
 Matches 131; Conservative 52; Mismatches 78; Indels 15; Gaps 6;  
 QY \* 5 TAFARLEGVALITGASGIGETAKLFSQHGAKVAIADYODELGHVSVEAIGTNSST- 63  
 26 TLYPKRLEGVAILITGAGHIGKATVMLFARHGATVVIADVNVAGSLAKSLSSHKTS 85  
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 86 MVAFISCDVSVADVENLVNVTIARYGLDILFNAGVLGQKHKSLIDFADFHDVHM 145  
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 04-MAY-1999; 99US-0132484.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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PR 14-MAY-1999; 99US-0134221.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
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PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
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PR 14-JUN-1999; 99US-0139119.  
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 PR 10-JUL-1999; 99US-0140362.  
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 PR 22-AUG-1999; 99US-0149930.  
 PR 23-AUG-1999; 99US-0150566.  
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 PR 25-AUG-1999; 99US-0151065.  
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 PR 30-AUG-1999; 99US-0151438.  
 PR 31-AUG-1999; 99US-0151930.  
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 PR 02-SEP-1999; 99US-0153070.  
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 PR 11-SEP-1999; 99US-0156596.  
 PR 12-SEP-1999; 99US-0157117.  
 PR 13-SEP-1999; 99US-0157753.  
 PR 14-SEP-1999; 99US-0157865.  
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 PR 16-SEP-1999; 99US-0158232.  
 PR 17-SEP-1999; 99US-0158369.  
 PR 18-SEP-1999; 99US-0159293.  
 PR 19-SEP-1999; 99US-0159294.  
 PR 20-SEP-1999; 99US-0159295.  
 PR 21-SEP-1999; 99US-0159329.  
 PR 22-SEP-1999; 99US-0159330.  
 PR 23-SEP-1999; 99US-0159331.  
 PR 24-SEP-1999; 99US-0159337.  
 PR 25-SEP-1999; 99US-0159338.  
 PR 26-SEP-1999; 99US-0159584.  
 PR 27-SEP-1999; 99US-0160741.  
 PR 28-SEP-1999; 99US-0160767.  
 PR 29-SEP-1999; 99US-0160768.  
 PR 30-SEP-1999; 99US-0160770.  
 PR 01-OCT-1999; 99US-0160814.  
 PR 02-OCT-1999; 99US-0160815.  
 PR 03-OCT-1999; 99US-0160980.  
 PR 04-OCT-1999; 99US-0160981.  
 PR 05-OCT-1999; 99US-0160989.  
 PR 06-OCT-1999; 99US-0161404.  
 PR 07-OCT-1999; 99US-0161405.  
 PR 08-OCT-1999; 99US-0161406.  
 PR 09-OCT-1999; 99US-0161359.  
 PR 10-OCT-1999; 99US-0161360.  
 PR 11-OCT-1999; 99US-0161361.  
 PR 12-OCT-1999; 99US-0161920.  
 PR 13-OCT-1999; 99US-0161992.  
 PR 14-OCT-1999; 99US-0161993.  
 PR 15-OCT-1999; 99US-0162142.

Query Match 42.9%; Score 597.5; DB 21; Length 283;

Best Local Similarity 47.0%; Pred No. 5.3e-51;

Matches 126; Conservative 45; Mismatches 86; Indels 11; Gaps 4;

Qy 9 RLEGVALITGASGIGETITAKLPFQHGAKVATADYODELGHVSVEAIGTSNHYHCD 68

Db 16 RLEGVALITGASGIGETITAKLPFQHGAKVATADYODELGHVSVEAIGTSNHYHCD 74



Qy	65	IHC	DVTNEDGVKNVDNTVSTY-GKLDIMFSGNAGI----	SDENRPRITDNEKADFERVLSV	120
Db	106	VRCD	SVSEDDVRAVDWALSRHGRLDVCNNAGVLGRQTFEARSILSFDAAEFDRVLRV	165	
Qy	121	NVTG	VELCHKHAARUMIPARSGNIIISTASLSSTWGGSSSHAYCGSKHAVLALTRNLAVEL	180	
Db	166	NALGA	ALGKWKHAARAWPRRAGSIVSVASVAAVLGGGLGPHAYTASRKHAIIVGLTKNAACEL	225	
Qy	181	QFGI	RVNCCLSPFGLPTA-----	LKKFSGIKNEEEFENV	216
Db	226	RAHG	VRVNCVSPFGVATPMLINAWRQGHDDATADADRLDLDLDTVPDQEVERKMEEV	285	
Qy	217	NFAG	NLKGPKFNVEDVANAALYLASDEARYVSGHNLFI	DGGFSVCNSVI	265
Db	286	RGLA	TLKGPTLRPRDIAEAVLEFLASDEARYISGHNLVVDGGVTTSRNLI	334	

Search completed: October 23, 2003, 12:48:25  
Job time : 87 secs



Db 106 VRCDSVEDDVRRAVDWALSRRHGRDLVYCNAGVLGRQTRAARSILSFDAABFDRVLRV 165  
 QY 121 NVTGVFLCMKHAARVMIPARSGNIISTASLSTMTGSGSHAYCGSKHVALTRNLAVEL 180  
 Db 166 NALGAALGMKHAARANAPRAGSIIVSVAVALGGLGPHAYTASKHAIVGLTKNAACEL 225  
 QY 181 GQFIRVNCILSPGLPTA-----LGKFGSGIKNEBEFENVI 216  
 Db 226 RAHGVRCVNSPFGVATPMLINAWRQGHDDATADADRLDLDLVTVPSQOEVEKMEEVV 285  
 QY 217 NFAGNLKPGKFNVEDVANAALYLASDEAKYVSGHNLFDIDGFGFVCSNVI 265  
 Db 286 RGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLI 334

RESULT 2  
 US-08-440-856A-4  
 ; Sequence 4, Application US/08440856A  
 ; Patent No. 5750873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DELLAPORTA, STEPHEN L.  
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
 ; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 2000 PENNSYLVANIA AVE. N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/440,856A  
 ; FILING DATE: 15-MAY-1995  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MILLMAN, ROBERT A.  
 ; REGISTRATION NUMBER: 36,217  
 ; REFERENCE/DOCKET NUMBER: 05463-20001.00  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 887-1517  
 ; TELEFAX: (202) 887-0763  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 333 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

Query Match 41.8%; Score 582.5; DB 1; Length 333;  
 Best Local Similarity 42.2%; Pred. No. 1.4e-54;  
 Matches 121; Conservative 50; Mismatches 89; Indels 27; Gaps 4;  
 QY 5 TAFARLEGKVALITGASGIGETTAKLFSOHGAKVAIADVQDELGHVSVVEAIGTSNSTY 64  
 Db 46 TPKPKRLXGKVAIVTGARGIGEAIVRLFKHGAKVVIADIDDAAGEALAAALG-PHVGF 104  
 QY 65 IHCDVTNEDGVQKAVNTVSTYTKGLDIFMSNAGI---SDPNRPRIIDNEKADPERVLSV 121  
 Db 105 VRCDSVEEDVERAVERAVARYGRDLVLCNNAGVLGRQTRAASKLSLSDAGEFDRVLRV 164  
 QY 122 VTGVFLCMKHAARVMIPARSGNIISTASLSTMTGSGSHAYCGSKHVALTRNLAVELG 181  
 Db 165 ALGALGMKHAALANTQRRAGSIIVSVAVALGGLGPHAYTASKHAIVGLTKNAACELG 224

QY 182 QFIRVNCILSPFGLPTAL-----GKFPS-----GIKNEBEFENVINVF 218  
 Db 225 AHGIRVNCISPFVGATPMLINAWRQGHDASTADDADIDLDIAVPSQOEVEKMEEVVRG 284  
 QY 219 AGNLKPGKFNVEDVANAALYLASDEAKYVSGHNLFDIDGFGFVCSNVI 265  
 Db 285 LATLKGATLRPRDIAEALFLASDDSRYSGHNLVVDGGVTTSRNLI 331

RESULT 3  
 US-08-440-856A-8  
 ; Sequence 8, Application US/08440856A  
 ; Patent No. 5750873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DELLAPORTA, STEPHEN L.  
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
 ; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 2000 PENNSYLVANIA AVE. N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/440,856A  
 ; FILING DATE: 15-MAY-1995  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MILLMAN, ROBERT A.  
 ; REGISTRATION NUMBER: 36,217  
 ; REFERENCE/DOCKET NUMBER: 05463-20001.00  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 887-1517  
 ; TELEFAX: (202) 887-0763  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 359 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide

US-08-440-856A-8  
 Query Match 35.9%; Score 500; DB 1; Length 359;  
 Best Local Similarity 38.8%; Pred. No. 1.3e-45;  
 Matches 112; Conservative 40; Mismatches 107; Indels 30; Gaps 5;  
 QY 5 TAFARLEGKVALITGASGIGETTAKLFSOHGAKVAIADVQDELGHVSVVEAIGTSNSTY 64  
 Db 50 TPKPKRLXGKVAIVTGARGIGEAIVRLFKHGAKVVIADIDDAAGEALAAALG-PXV 108  
 QY 65 IHCDVTNEDGVQKAVNTVSTYTKGLDIFMSNAGI---SDPNRPRIIDNEKADPERVLSV 120  
 Db 109 VRCDSVEXDXRVAXVXXKXRXGRDLVACNNAGVLGRQTRAAXSILSFDAKEXFDRVLRV 168  
 QY 121 NVTGVFLCMKHAARVMIPARSGNIISTASLSTMTGSGSHAYCGSKHVALTRNLAVEL 180  
 Db 169 NALGAALGMKHAAXAMXXRRAGSIIXSVASVAVLGGGLGPHAYTASKHAIVGLTKNAACEL 228  
 QY 181 GQFIRVNCILSPGLPTA-----LGKFGSGIKNEBEFENVI 216  
 Db 229 XH-GXRVNCXSPFGVATPMLINAWRQGHDXXTADXXDXDLDDXXVPSQOEVEKMEEVV 287  
 QY 217 NFAGNLKPGKFNVEDVANAALYLASDEAKYVSGHNLFDIDGFGFVCSNVI 265





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; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
; FILE REFERENCE: BC1001 US NA
; CURRENT FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PR1
; ORGANISM: Brevibacterium sp HCU
; US-09-954-314-14

Query Match 26.5%; Score 369; DB 4; Length 256;
Best Local Similarity 35.7%; Pred. No. 1.2e-31;
Matches 91; Conservative 55; Mismatches 101; Indels 8; Gaps 5;

QY 10 RLEKVALITGGASGIGETTAKLFSOHGAKVAIADVDQELGHSVVEAIGTSN--STYIHC 67
DB 3 RLGKVAIVITGGAAGMRIGQSELYASEGAQVAVDVNQEGRATADAIRASGGVANYWKL 62
QY 68 DVNEDGVKNVAVNTVSTYCKLDMFNSNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFL 127
DB 63 DVSESEVEIWSDIKREKAINLVNNAAGVTGADKPTHEIDER-DLDELVLSDVVKGVFP 121
QY 128 CMKHAARVMPARSNGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLNLAVALGQFGRV 187
DB 122 MTKHCIPYFKQAGGAIIVNFAIYGLVGSQELTPYHAAKGAVALTKQDATTYGPSNIRV 181
QY 188 NCLSPGLPTALGKKSFGKNEEENPVNFAGNLKGPKNV---EDVANAALYLASDEA 244
DB 182 NAVAPGTILTPVKEL-GRGPDGLDGYTKLMG-AGPLGRVTPTEVAAATFLASEA 239
QY 245 KYVSGHNLFTDGGFS 259
DB 240 SFTGAVLPVDDGGYT 254

RESULT 8
US-09-198-452A-309
; Sequence 309, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 309
; LENGTH: 251
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-309

Query Match 25.6%; Score 357; DB 4; Length 251;
Best Local Similarity 33.5%; Pred. No. 2.2e-30;
Matches 87; Conservative 53; Mismatches 92; Indels 28; Gaps 6;

QY 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAIADVDQELGHSVVEAI-GTSNS-TYIHC 68
DB 8 LVGKVVITGSGRGIGLVKLFLENGADVEIWLNEERGQAVIESLTGLGSEVSFARV 67
QY 69 VTNEDGVKNVAVNTVSTYCKLDMFNSNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFLC 128
DB 68 VSHNGGVCKVQKFLDKHKNKIILVNNAGITRDN--LLMRSEDDQSVISTNLISLYT 125
QY 129 MKHAARVMPARSNGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLNLAVALGQFGRV 188
DB 126 CSSVIRHMKARSGSLINVASIVAKIGSAGQNTYAAKAGATIAFKSLAKEVAARNIRVN 185
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QY 189 CLSPFGLPTALGKKSFGKNEEENPVNFAGNLK-----GPKFNVEDVANAALYL 239
DB 186 CLAPGFI-----ETDMSVLN--DNLKAEMWKSIPILGRAGTPEEDVARVALFL 230
QY 240 ASDEAKYVSGHNLFTDGGFS 259
DB 231 ASQLSSYMTAQTLVVDGGLT 250

RESULT 9
US-09-328-352-7731
; Sequence 7731, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7731
; LENGTH: 261
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7731

Query Match 25.3%; Score 352; DB 4; Length 261;
Best Local Similarity 34.5%; Pred. No. 8.2e-30;
Matches 89; Conservative 53; Mismatches 104; Indels 12; Gaps 4;

QY 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAIADVDQELGHSVVEAIGTS--NSTYIHC 68
DB 5 LDGKVAIVITGSGASGIGLEIAKFAQEGAKVVISDMNAEKCOETASSLKERGFDAISAPCD 64
QY 69 VTNEDGVKNVAVNTVSTYCKLDMFNSNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFLC 128
DB 65 VTDEDAYKQAIETQKTFTGVDILINNAGFQ--HVAPIEEFPPIAVFQKLVQVWMLTGAFIG 122
QY 129 MKHAARVMPARSNGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLNLAVALGQFGRV 188
DB 123 IKHVFPIKRAQKYGRILNINWASINGLIGFAGKAGYNSAKHGVIGLTKVAALECARDGITVN 182
QY 189 CLSPFGLPTALGK-----KFSGKNEEENPVNFAGNLKGPKNVEDVANAALYLAS 241
DB 183 ALCPGVYDTPLVRGQIADLAKTRNVSLDSELDVI-LAMVPQKLLSVEEADIYTIELAS 241
QY 242 DEAKYVSGHNLFTDGGFS 259
DB 242 SKAGGVITGQAVVMDGGYT 259
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RESULT 10
US-09-363-189B-6
; Sequence 6, Application US/09363189B
; Patent No. 6242228
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZAKI, KENZO
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PR1
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-940-019-29

Query Match      24.5%; Score 341.5; DB 4; Length 261;
Best Local Similarity 34.4%; Pred. No. 1.1e-28;
Matches 93; Conservative 50; Mismatches 98; Indels 29; Gaps 10;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTVI 65
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 LKGVVAITGAASGLGKAMAIRFGKEQAKVINYNSKQDPNEVKEEVIKAGG--EAVVV 62
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 66 HCDVTNEDGVKNADVNTVSTYKLDIMFSNAGISDPNRPRIIDNEK--ADFERVLSVNTT 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 63 QGDTVTEEDVKNIVQTAIRKEFGTLDIMINNAGLENP---VPSHEMLPKDWDKVGITNLT 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 GVFLCMKHAARVMIPAR-SGNIISTASISSTWGGSSHAYCGSKHVALATRLNLAVELGQ 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 119 GAFGLSREAIKYFVENDIKGNVINNSSVHEVWPFLFVHYAASKGKIKMTETLALEYAP 178
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 183 FGIRVNCCLSPFGLPTAL-GKKESGINKNEEFENFVINFAGNLKGPKNVEDVANAALYLAS 241
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 179 KGIRVNNIGPAINTPINAEKFADEPKQADVESMIPM-GYIGEP-----EETAAVAWLAS 233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 242 DEAKYVSGHNLFIDGFSVCNSVIKVFQYP 271
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 234 KEASYVTGITLFDAGGMT-----QYP 254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-940-037A-29
; Sequence 29, Application US/09940037A
; Patent No. 6485948
; GENERAL INFORMATION:
; APPLICANT: Kimoto, No. 6485948ihiro
; APPLICANT: Mitsuhashi, Kazuo
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID
; TITLE OF INVENTION: ENZYME
; FILE REFERENCE: 06501-050001
; CURRENT APPLICATION NUMBER: US/09/940,037A
; PRIOR FILING DATE: 2000-08-27
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0, reformatted using WordPerfect 5.1
; SEQ ID NO 29
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-940-037A-29

Query Match      24.5%; Score 341.5; DB 4; Length 261;
Best Local Similarity 34.4%; Pred. No. 1.1e-28;
Matches 93; Conservative 50; Mismatches 98; Indels 29; Gaps 10;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTVI 65
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 LKGVVAITGAASGLGKAMAIRFGKEQAKVINYNSKQDPNEVKEEVIKAGG--EAVVV 62
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 66 HCDVTNEDGVKNADVNTVSTYKLDIMFSNAGISDPNRPRIIDNEK--ADFERVLSVNTT 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 63 QGDTVTEEDVKNIVQTAIRKEFGTLDIMINNAGLENP---VPSHEMLPKDWDKVGITNLT 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 GVFLCMKHAARVMIPAR-SGNIISTASISSTWGGSSHAYCGSKHVALATRLNLAVELGQ 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 119 GAFGLSREAIKYFVENDIKGNVINNSSVHEVWPFLFVHYAASKGKIKMTETLALEYAP 178
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 183 FGIRVNCCLSPFGLPTAL-GKKESGINKNEEFENFVINFAGNLKGPKNVEDVANAALYLAS 241
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5042

Query Match      23.8%; Score 331.5; DB 4; Length 267;
Best Local Similarity 32.1%; Pred. No. 1.4e-27;
Matches 88; Conservative 55; Mismatches 96; Indels 35; Gaps 9;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAIADVQDELGHVSVEAIGTSNSTY----- 64
Db 9 LENKVVLIITGAATGIGKIAENFGKAKAVI-NYRSDRHHSEIEEIKQTVAKFGGQTLA 67
Qy 65 IHCVDVTNEDGVKNADVNTVSTYKLDIMFSNAGI--SDPNRPRIIDNEKADFERVLSVNV 122
Db 68 VQGDVSIEEDIKRMIEITTIINHFGLDIIINNAGPENSIPTHEMSID---DWQKVIDINL 123
Qy 123 TGVFLCMKHAARVMIPAR-RSGNIISTASISSTWGGSSHAYCGSKHVALATRLNLAVELG 181
Db 124 TGAFGSRETINQFLKENKGTIINISSVHDTIPWPNVHYAASKGGLKMMETMSMEYA 183
Qy 182 QGIRVNCCLSPFGLPTALGK-KFSGIKNEEFENFVINFAGNLKGPK---FNVEDVANAAL 237
Db 184 QYGIIRINNISPGAIVTEHTKEKSPDPTTREETIKMI-----PAREIGNAQDVANAVL 235
Qy 238 YLASDEAKYVSGHNLFIDGFSVCNSVIKVFQYP 271
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 236 FLSSDLASYIHGTTLYVDGG-----MMNYP 260
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: October 23, 2003, 12:52:01
Job time : 30 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:50:44 ; Search time 68 Seconds  
(without alignments)  
672.305 Million cell updates/sec

Title: US-09-673-918A-2

Perfect score: 1393

Sequence: 1 MQLRTAFARLEGKVALITG.....IDGFSVCNSVIKVFQYPS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	88.5	276	10	US-09-944-160-24
2	487.5	35.0	272	12	US-10-242-224-8
3	432	31.0	253	9	US-09-815-242-11842
4	382	27.4	258	15	US-10-156-761-11335
5	380.5	27.3	263	15	US-10-156-761-14255
6	369	26.5	256	10	US-09-954-314-14
7	369	26.5	256	15	US-10-230-562-14
8	349.5	25.1	262	9	US-09-802-853-6
9	349.5	25.1	262	15	US-10-307-385-6
10	343.5	24.7	267	10	US-09-773-748-1
11	343.5	24.7	267	12	US-10-327-726-1
12	341.5	24.5	261	10	US-09-940-037A-29
13	332	23.8	245	12	US-10-237-496-82
14	332	23.8	245	12	US-10-242-074-82
15	332	23.8	245	12	US-10-242-505-82

16	332	23.8	245	12	US-10-242-574-82	Sequence 82, Appl
17	332	23.8	245	12	US-10-243-261-82	Sequence 82, Appl
18	332	23.8	245	12	US-10-243-282-82	Sequence 82, Appl
19	332	23.8	245	12	US-10-243-402-82	Sequence 82, Appl
20	332	23.8	245	12	US-10-243-431-82	Sequence 82, Appl
21	332	23.8	245	12	US-10-245-164-82	Sequence 82, Appl
22	332	23.8	245	12	US-10-244-972-82	Sequence 82, Appl
23	332	23.8	245	12	US-10-197-942-82	Sequence 82, Appl
24	332	23.8	245	12	US-10-238-196-82	Sequence 82, Appl
25	332	23.8	245	12	US-10-245-013-82	Sequence 82, Appl
26	332	23.8	245	15	US-10-245-103-82	Sequence 82, Appl
27	332	23.8	245	15	US-10-245-107-82	Sequence 82, Appl
28	332	23.8	245	15	US-10-245-143-82	Sequence 82, Appl
29	332	23.8	245	15	US-10-245-771-82	Sequence 82, Appl
30	332	23.8	245	15	US-10-245-851-82	Sequence 82, Appl
31	332	23.8	245	15	US-10-245-883-82	Sequence 82, Appl
32	332	23.8	245	15	US-10-237-535-82	Sequence 82, Appl
33	332	23.8	245	15	US-10-238-183-82	Sequence 82, Appl
34	332	23.8	245	15	US-10-238-283-82	Sequence 82, Appl
35	332	23.8	245	15	US-10-238-370-82	Sequence 82, Appl
36	332	23.8	245	15	US-10-245-055-82	Sequence 82, Appl
37	332	23.8	245	15	US-10-245-147-82	Sequence 82, Appl
38	332	23.8	245	15	US-10-245-730-82	Sequence 82, Appl
39	332	23.8	245	15	US-10-245-739-82	Sequence 82, Appl
40	332	23.8	245	15	US-10-246-210-82	Sequence 82, Appl
41	332	23.8	245	15	US-10-239-196-82	Sequence 82, Appl
42	332	23.8	245	15	US-10-243-024-82	Sequence 82, Appl
43	332	23.8	245	15	US-10-243-409-82	Sequence 82, Appl
44	332	23.8	245	15	US-10-245-621-82	Sequence 82, Appl
45	332	23.8	245	15	US-10-245-880-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

US-09-944-160-24  
; Sequence 24, Application US/09944160  
; Patent No. US20020174452A1  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, No. US20020174452A1man  
; APPLICANT: Davin, Laurence  
; APPLICANT: .. Huang, Ning  
; TITLE OF INVENTION: Monocot Seeds with Increased Lignan  
; TITLE OF INVENTION: Content  
; FILE REFERENCE: WSUR117983  
; CURRENT APPLICATION NUMBER: US/09/944,160  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/230,632  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: secoisolaricresinol dehydrogenase amino acid  
; OTHER INFORMATION: sequence from plasmid pAPI249  
US-09-944-160-24

Query Match	88.5%	Score 1233;	DB 10;	Length 276;
Best Local Similarity	88.2%	Pred. No. 3.7e-115;		
Matches 240;	Conservative 14;	Mismatches 18;	Indels 0;	Gaps 0;
Qy	2	QLRTAFARLEGKVALITGASGIGETTAKLFQHGAKVAIADVDQLGHSVWEAIGTSN	61	
Db	5	QLRTAFARLEGKVALITGASGIGETTAKLFQHGAKVAIADVDQLGHSVWEAIGLSN	64	
Qy	62	STVHCDDVTNEDGVKNAVDNTVSTYTKLDMFNSNAGISDPNRPRIIDNEKADFERVLSVN	121	
Db	65	STVHCDDVTNEDGVKNAVDNTVSTYTKLDMFNNAGISDPYKPRVIDNEKADFERVLSVN	124	

Qy 122 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMGSSSHAYCGSKHVALTRNLAVEIG 181  
Db 125 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMGSSSHAYCGSKHVALTRNLAVEIG 184  
Qy 182 QGIRVNCISLPGPLTALGKFKSGIKNEEFENVINPAGNLKPGKPNVEDVANAALYLAS 241  
Db 185 QGIRVNCISLPGPLTALGKFKSGIKNEEFENVINPAGNLKPGKPNVEDVANAALYLAS 244  
Qy 242 DEAKYVSGHNFIDGFSVCNSVTKVQYFDS 273  
Db 245 DEAKYVSGHNFIDGFSVCNSVTKVQYFDS 276

RESULT 2

US-10-342-224-8  
; Sequence 8, Application US/10342224  
; Publication No. US20030162294A1  
; GENERAL INFORMATION:  
; APPLICANT: Nathalie Verbruggen  
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress  
; FILE REFERENCE: CNN-012US  
; CURRENT APPLICATION NUMBER: US/10/342,224  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US/09/762,154  
; PRIOR FILING DATE: 2002-02-02  
; PRIOR APPLICATION NUMBER: EP 98202634.6  
; PRIOR FILING DATE: 1998-08-04  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-342-224-8

Query Match 35.0%; Score 487.5; DB 12; Length 272;  
Best Local Similarity 44.2%; Pred. No. 1.6e-40;  
Matches 118; Conservative 45; Mismatches 91; Indels 13; Gaps 7;  
Qy 9 RLREGKVALITGGASIGETAKLFSQHGAKVAIADVDDELGHVSVEAI--GTSNSTVI 68  
Db 6 KRLFEKVALITGGASIGETAKLFSQHGAKVAIADVDDELGHVSVEAI--GCVVHCD 62  
Qy 69 VTNEDGVKNADVNTSTYTKLIDMFNSAGISDPNRPRIIDNEKADPERVLSVNVTVGVL 128  
Db 63 VSKEADVEAAVELAMRRKGRLDVNFNAGMS-LNEGSIMGMDVDMVKNLVSNNVNGVLHG 121  
Qy 129 MKHAARVMIP-ARSGNIISTASLSSTMGSSSHAYCGSKHVALTRNLAVEIGQFGRV 187  
Db 122 IKHAAMIKGKGSGIISCTSSSGLMGLGCHAYTLKGGINGVVRTTECELGSHGIRV 181  
Qy 188 NCLSPFGLPT----ALGKFKSGIK-NEEFENVINPAGN-LKGPKNVEDVANAALYLA 240  
Db 182 NSISPHGVTDILVNAYRKFLNNDKLVNAEYTDIIAEKGSILTGAGTVEDVAAQALFLA 241  
Qy 241 SDEAK-YVSGHNFIDGFSVCNSVIK 266  
Db 242 SQESSGFIHNLVVDGGYTSATSMR 268

RESULT 3

US-09-815-242-11842  
; Sequence 11842, Application US/09815242  
; Patent No. US2002061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseibeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11842  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-11842  
Query Match 31.0%; Score 432; DB 9; Length 253;  
Best Local Similarity 37.5%; Pred. No. 5.2e-35;  
Matches 95; Conservative 52; Mismatches 98; Indels 8; Gaps 4;  
Qy 8 ABRLGKVALITGGASIGETAKLFSQHGAKVAIADVDDELGHVSVEAI--GTSNSTVI 65  
Db 2 SKLLSGQVALYTGGAAGIGRATALAPAAAGVKVVVADLDSAGGEGTVEAIROAGGEALFI 61  
Qy 66 HDVTNEDGVKNADVNTSTYTKLIDMFNSAGISDPNRPRIIDNEKADPERVLSVNVTVG 125  
Db 62 RCDVTRDAEVAALVEGCAAYGRLDYAFNNAGI-EIEQGLADGNEAEFPDAIVNVNKG 120  
Qy 126 FLCMKHAARVMIPARSGNIISTASLSSTMGSSSHAYCGSKHVALTRNLAVEIGQF 185  
Db 121 WLCMKHQIPLMUAQGGGAIVNTASVAGLGAAPKMSIYAASKHAVIGLTKSAALEYAKKGI 180  
Qy 186 RVNCLSPFGLPTALGKK-FSGIKNEEFENVINPAGNLKGPKNVEDVANAALYLASDEA 244  
Db 181 RVNAVCEPAVIDTDMFRRAYEADPRKAEFAAMHPLGRVG----RVBEIAAAVLYLCCDNA 236  
Qy 245 KYVSGHNFIDGG 257  
Db 237 GFTTGIALPVDGG 249

RESULT 4

US-10-156-761-11335  
; Sequence 11335, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109

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; SEQ ID NO 11335
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11335

Query Match      27.4%; Score 382; DB 15; Length 258;
Best Local Similarity 36.8%; Pred. No. 5.4e-30;
Matches 96; Conservative 46; Mismatches 109; Indels 10; Gaps 4;

Qy 10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNITYHCDV 69
Db 3 KLDGRVVLISGAARQGEQEARLVEBGAQVVDVLDQGEALAKSIG---ARYVHLDV 59
Qy 70 TNEGVKNVADNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLCM 129
Db 60 GREDDWQAQAVTVAKDAYGHIDGLVNNAGILRFN--DLVGTPLAEFQIQVQVQGVFLGI 117
Qy 130 KHAARVMIPARSGNIISTASLSSTWGGSSHAYCGSKHAVLALTRNLAVELGQFGIRWC 189
Db 118 KTVAPEIEAAGGGTIVNTASVAGLTGMAYVGAYTATKHAIVGLTRVAALELAACKIRVNA 177
Qy 190 LSPGGLTALGKKFS---GKNEEFENFVNFAGNL--KGPKNFVEDVANAALYLASDEA 244
Db 178 VCPGAIDTAMNPQSLDPGADPEETARALSSELYGLRVLPLGRLGRPPEVARLALFLSGEDS 237
Qy 245 KYVSGHNLFTIDGGFSCNVI 265
Db 238 SYITGQFVIDGGWLAGVSVI 258

RESULT 5
US-10-156-761-14255
; Sequence 14255, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14255
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14255

Query Match      27.3%; Score 380.5; DB 15; Length 263;
Best Local Similarity 35.3%; Pred. No. 7.9e-30;
Matches 89; Conservative 48; Mismatches 108; Indels 7; Gaps 3;

Qy 9 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNITYHCD 68
Db 11 RRLVGRVAVITGAGSGIGLATAERLASGHHVCGDIDEVSGKAAADEVG---GTFVQVD 67
Qy 69 VTNEGVKNVADNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLC 128
Db 68 VTDAEQVEALPRTAYDTYGSVDIAFNAGISFPDDDSILETGLAWKRVQEVNLTSVLC 127
Qy 129 MKHAARVMIPARSGNIISTASLSSTWGGSSH-AYCGSKHAVLALTRNLAVELGQFGIRV 187
Db 128 CKAAPYMRQRGRSIIINTASVARMGAATSQISYTASKGVGLAWSRELGVQFPAREGIRV 187
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Qy 188 NCLSPFGLPTALGKFKSGIKNEEEFENVNFAGNLKGPKNFVEDVANAALYLASDEAKYV 247
Db 188 NALCPGPNVTPLLQELFPAKDPERAAARLVHP---VGRFAEAEDEIAAAVAFLASDDSSFV 244
Qy 248 SGHNLFTIDGGFS 259
Db 245 NATDFLVDGGIS 256

RESULT 6
US-09-954-314-14
; Sequence 14, Application US/09954314
; Patent No. US20020127666A1
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; APPLICANT: Brzostowicz, Patricia C.
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
; FILE REFERENCE: BC1001 US NA
; CURRENT APPLICATION NUMBER: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Brevibacterium ep HCU
US-09-954-314-14

Query Match      26.5%; Score 369; DB 10; Length 256;
Best Local Similarity 35.7%; Pred. No. 1.1e-28;
Matches 91; Conservative 55; Mismatches 101; Indels 8; Gaps 5;

Qy 10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN--STYIHC 67
Db 3 RLGGKVAIVTGGAAAGMGRISQSELYASEGAQVAVVDVNEQEGRATADAIRASGGVANYWKL 62
Qy 68 DVTNEDGVKNVADNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFL 127
Db 63 DVSDSEVEIVVSDIAKRFAGIINVLVNNAVGTGADKPTHEIDER-DLDLVLSDVDKGVFF 121
Qy 128 CMKHAARVMIPARSGNIISTASLSSTWGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
Db 122 MTKHCIPYFKQAGGAIIVNFASIVGLVGSQELTPYHAAKGAVALTKQDATTYGPSNIRV 181
Qy 188 NCLSPFGLPTALGKFKSGIKNEEEFENVNFAGNLKGPKNV---EDVANAALYLASDEA 244
Db 182 NAVAPGTTILPLVKEL--GSRGPDGLDGYTKLMG-AKHPGLRGVGTPEEVAATLFLASEEA 239
Qy 245 KYVSGHNLFTIDGGFS 259
Db 240 SFTGAVLPVDGGYT 254
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```
RESULT 7
US-10-230-562-14
; Sequence 14, Application US/10230562
; Publication No. US20030113886A1
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; APPLICANT: Brzostowicz, Patricia C.
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID
; FILE REFERENCE: BC-1001
; CURRENT APPLICATION NUMBER: US/10/230,562
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
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; LENGTH: 256
; TYPE: PRT
; ORGANISM: Brevibacterium sp HCU
US-10-230-562-14

Query Match      26.5%; Score 369; DB 15; Length 256;
Best Local Similarity 35.7%; Pred. No. 1.1e-28;
Matches 91; Conservative 55; Mismatches 101; Indels 8; Gaps 5;

Qy 10 RLEGKVALITGASGIGETTAKLFSOHGAKVAIADVQDELGHSVVEAIGTSN--STYIHC 67
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 3 RLGGKVAVITGAAGMGRISQSELYASEGAQVAVVDVNEQEGRATADAIRASGCVANYWL 62
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 68 DVTNEDGVKNADVNTVSTYKGLDIMFSNAGISDPNRIIDNEKADPERVLSVNVTVGFL 127
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 63 DVSDESEIVEIVSDIAKRFAGINLVNNAVGTGADKPTHEIDER-DLDELVLSVDVKGVEF 121
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 128 CMKHAARVMIPARSGNIISTASLSMTGGSSSHAYCGSKHVALTRNLAVELGQFGIRV 187
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 122 MYKHCIPYEQAGGGAIVNFASIVGLVGSQELTPYHAAKGAVALTKQDAVTYGPSNIRV 181
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 188 NCLSPFGLTALGKFGSGIKNEEFENVINPAGNLKGPKNV---EDVANAALYLASDEA 244
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 182 NAVAPOTILPLVKEL-GSRGPDGLDGYTKLMG-AKHPLGRVGTPEEVAATLFLASEEA 239
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 245 KYVSGHNLFDGGFS 259
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 240 SFITGAVLPVDGGYT 254
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
US-09-802-853-6
; Sequence 6, Application US/09802853
; Patent No. US20010034049A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZEKI, KENZO
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT FILING DATE: 2001-03-12
; PRIOR FILING DATE: 1999-07-29
; PRIOR FILING DATE: 1999-07-29
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
US-09-802-853-6

Query Match      25.1%; Score 349.5; DB 9; Length 262;
Best Local Similarity 31.2%; Pred. No. 9.9e-27;
Matches 83; Conservative 55; Mismatches 107; Indels 21; Gaps 6;

Qy 8 ARLEGKVALITGASGIGETTAKLFSOHGAKVAIADVQDEL---GHSVVEAIGTSNSTY 64
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 2 SKFNGKVCVLTGAGNIGLATALRLAEGTAIALLDMNREALEKASVREKGVARSY 61
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 65 IHCDDVTNEDGVKNADVNTVSTYKGLDIMFSNAGISDPNRIIDNEKADPERVLSVNVTVG 124
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 V-CDDTSEEAVIGTVDSVVRDFGKIDFLFNNAAGYQAFAP-VQDYPSPDDFARVLTINVTG 119
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 125 VFLCMKHAARVMIPARSGNIISTASLSMTGGSSSHAYCGSKHVALTRNLAVELGQFG 184
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 AFHVLKAVSRQMTQNYGRIVNTASMGVKKPPNMAAYGASKGAIITALTETAALDLAPYN 179
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 185 IRVNCCLSP-----FGLPTALGKFGSGIKNEEFENVINPAGNLKGPKNV-NVED 231
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 232 VANAALYLASDEAKYVSGHNLFDGG 257
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 237 IPGVVAFLLGDDSSSFMTGVNLPFIAG 262
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 10
US-09-773-748-1
; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Wada, Masaru
; TITLE OF INVENTION: Levodione reductase gene and use thereof
; FILE REFERENCE: Levodione reductase
; CURRENT APPLICATION NUMBER: US/09/773,748
; CURRENT FILING DATE: 2001-01-31
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
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FILE REFERENCE: P3630R1C4  
CURRENT APPLICATION NUMBER: US/10/237.496  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 82  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-237-496-82

Query Match 23.8%; Score 332; DB 12; Length 245;  
Best Local Similarity 33.5%; Pred. No. 5.1e-25;  
Matches 85; Conservative 57; Mismatches 98; Indels 14; Gaps 7;  
Qy 10 RUEGKVALITGASIGETTAKLFQSGAKVAIADVODELGHSVVEAIGTSNSTYIHCDV 69  
Db 3 RLDGKVIILTAQAQIGQAALAFAREGAKVIATDINESKQLSEKYPGIGQTRV---LDV 59  
Qy 70 TNEGDKVNAVNTYSTYKGLDIMFSNAGISDPNRPRIIDNEKADFRLVLSVNVTVGLCM 129  
Db 60 TK----KKQIDQFASEVERLDVLENAVGF--VHHGTVLDCDEEKDWFMSNLRVSRMYLMI 113  
Qy 130 KHAARVMIIPARSNGIISTASLSSTMTGGSSH-AYCGSKHVALALTRNLAVELGQFGIRVN 188  
Db 114 KAPLPKMLAQKSGNIINSSVASSVKGVNVRCVYSTTKAAVIGLTKSLAADFTQQGIRCN 173  
Qy 189 CLSPGGLPT-ALGKKFSGIKNEEFENVINPAGNLKGPKE-NVEDVANAALYLASDEAKY 246  
Db 174 CVCFGTVDTPSLQERIQARGNPEARN--DFLKKQKTGRFATAEBIAMLCLVYLASDESAY 231  
Qy 247 VSGHNLFDGGFSV 260  
Db 232 VTGNPVIIDGGWSL 245

RESULT 14  
US-10-242-074-82  
Sequence 82, Application US/10242074  
Publication No. US20030138897A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watande, Colin  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C19  
CURRENT APPLICATION NUMBER: US/10/242.074  
CURRENT FILING DATE: 2002-09-11  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 82  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-242-074-82

Query Match 23.8%; Score 332; DB 12; Length 245;  
Best Local Similarity 33.5%; Pred. No. 5.1e-25;  
Matches 85; Conservative 57; Mismatches 98; Indels 14; Gaps 7;  
Qy 10 RUEGKVALITGASIGETTAKLFQSGAKVAIADVODELGHSVVEAIGTSNSTYIHCDV 69  
Db 3 RLDGKVIILTAQAQIGQAALAFAREGAKVIATDINESKQLSEKYPGIGQTRV---LDV 59  
Qy 70 TNEGDKVNAVNTYSTYKGLDIMFSNAGISDPNRPRIIDNEKADFRLVLSVNVTVGLCM 129  
Db 60 TK----KKQIDQFASEVERLDVLENAVGF--VHHGTVLDCDEEKDWFMSNLRVSRMYLMI 113  
Qy 130 KHAARVMIIPARSNGIISTASLSSTMTGGSSH-AYCGSKHVALALTRNLAVELGQFGIRVN 188  
Db 114 KAPLPKMLAQKSGNIINSSVASSVKGVNVRCVYSTTKAAVIGLTKSLAADFTQQGIRCN 173  
Qy 189 CLSPGGLPT-ALGKKFSGIKNEEFENVINPAGNLKGPKE-NVEDVANAALYLASDEAKY 246  
Db 174 CVCFGTVDTPSLQERIQARGNPEARN--DFLKKQKTGRFATAEBIAMLCLVYLASDESAY 231  
Qy 247 VSGHNLFDGGFSV 260  
Db 232 VTGNPVIIDGGWSL 245

RESULT 15  
US-10-242-505-82  
Sequence 82, Application US/10242505  
Publication No. US20030138898A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watande, Colin  
APPLICANT: Wood, William

```

; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C25
; CURRENT APPLICATION NUMBER: US/10/242,505
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 82
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-242-505-82

Query Match      23.8%; Score 332; DB 12; Length 245;
Best Local Similarity 33.5%; Pred. No. 5.1e-25;
Matches 85; Conservative 57; Mismatches 98; Indels 14; Gaps 7;

Qy 10 RLEGKVALITGCGAGIGETTAKLFSQHGAKVAIADVQDELGHSVVEALGTSNSTYIHCDV 69
Db 3 RLDGKVIILTAAGIGQAALAFAREGAKVIATDINESKLOELEKYPGIQTRV---LDV 59

Qy 70 TNEDGVKNVADNTYSTYKLDIMFNSAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLCM 129
Db 60 TK---KKQIQFASEVERLDVLFNVAGF--VHHGTVLDCCEKDWDFSMNLNVRSMYIMI 113

Qy 130 KHAARVMTPARSGNIISTASLSTMGSSSH-AYCGSKHAVLALTRNLAVELQGFGRVN 188
Db 114 KAFLPKMLAQSGNIINMSSVASSVKGVYVRCVYSTTKAAVIGLTKSIAADFIQGGIRCN 173

Qy 189 CLSPFGLPT-ALGKKFSGIKNEEFENVINFAGNLKPKF-NVEDVANAALYLASDEAKY 246
Db 174 CVCFGTVDTPSLQRIQARGNPEARN--DFLKRQKQTRGFATBEIAMLCVYLASDESAY 231

Qy 247 VSGHNLFTIDGGFSV 260
Db 232 VTGNPVIIDGGWSL 245
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Search completed: October 23, 2003, 13:00:39  
Job time : 69 secs

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A;Accession: T02257  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A;Residues: 1-284 <HER>  
A;Cross-references: EMBL:AJ231177; NID:g2739278; PIDN:CAA1153.1; PID:g2739279  
A;Experimental source: cultivar SNN; tissue-type leaf  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.2%; Score 685; DB 2; Length 284;  
Best Local Similarity 53.8%; Pred. No. 6.8e-47;  
Matches 140; Conservative 37; Mismatches 83; Indels 0; Gaps 0;

QY 3 LRTAFARLEKVALITGGASGIGETTAKLFQHGAKVAIADVDDELGHVSVEAIGTSNS 62  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 6 LPSPIAKRLKGVKALITGGASGIGATTARLFVQHGAQVTDIADINLGTSLSVOEIGNHT 65  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 63 TVIHCDVTNEDGVKNADVNTVSTYGKLDIMFMSNAGISDPNPRIIDNEKADFERVLSNVV 122  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 66 IFVHCNAVESDVQNVDATIAFKGLDIMFSNAGIGKSIISSILDVDYDIKTVPDNI 125  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 123 TGCVFLCMKHAAVRMIPARSNGIIISTASLGSTWGGSSHAYCGSKHAVLATRNLAIVELGQ 182  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 126 VGAFACGHAARVMIPFKGSIIIFTASAATVSGVIPHAYSASKGAVLGFSKGIIVELCK 185  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 183 GDIRVNCPLSPCLTALCKFKSFGKNEEFENVINFAGNLKPKNVEDVANALVLASD 242  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 186 YGIRVCNPSPHYISTPLVNALGIAERAEIKWFPAAGNLKGALLDEEVAKAVLYLASD 245  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 243 EAKYVSGHNLFIDGFSVCN 262  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 246 DSKYVSGNMVLIDGGFTTN 265  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3  
F95653  
hypothetical protein F9K6.3 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
R;Theologian: F95653  
C;Accession: A96563  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
anzen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Rooney, T.; Rowley, D.; Sakano, H.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; PMID:21016719; PMID:11130712  
A;Accession: F95653  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-285 <STO>  
A;Cross-references: GB:A8005173; NID:g10645436; PIDN:AAG21552.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: F9K6.3  
A;Map position: 1  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 47.3%; Score 658.5; DB 2; Length 285;  
Best Local Similarity 50.9%; Pred. No. 8.6e-45;  
Matches 139; Conservative 43; Mismatches 78; Indels 13; Gaps 5;

QY 8 ARRLKGVKALITGGASGIGETTAKLFQHGAKVAIADVDDELGHVSVEAI--GTNST-- 63  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 15 SQRLGKVLTGGATIGSIGSVLRFPKGAQVCIVDQLDDGVBCKSLRGSEKETAF 74  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 64 YTHCDVTNEDGVKNADVNTVSTYGKLDIMFMSNAGISDPNPRIIDNEKADFERVLSNVV 123  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 75 FTGHGVRVEDDISNAVDFAVKNFETDLILNAGLCGAPCPDIRNYSISEFMFTFDVNVK 134  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 124 GVFLCMKHAAVRMIPARSNGIIISTASLGSTWGGSSHAYCGSKHAVLATRNLAIVELGQF 193  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

A;Accession: T02257  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A;Residues: 1-284 <HER>  
A;Cross-references: EMBL:AJ231177; NID:g2739278; PIDN:CAA1153.1; PID:g2739279  
A;Experimental source: cultivar SNN; tissue-type leaf  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.2%; Score 685; DB 2; Length 284;  
Best Local Similarity 53.8%; Pred. No. 6.8e-47;  
Matches 140; Conservative 37; Mismatches 83; Indels 0; Gaps 0;

QY 3 LRTAFARLEKVALITGGASGIGETTAKLFQHGAKVAIADVDDELGHVSVEAIGTSNS 62  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 6 LPSPIAKRLKGVKALITGGASGIGATTARLFVQHGAQVTDIADINLGTSLSVOEIGNHT 65  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 63 TVIHCDVTNEDGVKNADVNTVSTYGKLDIMFMSNAGISDPNPRIIDNEKADFERVLSNVV 122  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 66 IFVHCNAVESDVQNVDATIAFKGLDIMFSNAGIGKSIISSILDVDYDIKTVPDNI 125  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 123 TGCVFLCMKHAAVRMIPARSNGIIISTASLGSTWGGSSHAYCGSKHAVLATRNLAIVELGQ 182  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 126 VGAFACGHAARVMIPFKGSIIIFTASAATVSGVIPHAYSASKGAVLGFSKGIIVELCK 185  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 183 GDIRVNCPLSPCLTALCKFKSFGKNEEFENVINFAGNLKPKNVEDVANALVLASD 242  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 186 YGIRVCNPSPHYISTPLVNALGIAERAEIKWFPAAGNLKGALLDEEVAKAVLYLASD 245  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 243 EAKYVSGHNLFIDGFSVCN 262  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 246 DSKYVSGNMVLIDGGFTTN 265  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3  
F95653  
hypothetical protein F9K6.3 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
R;Theologian: F95653  
C;Accession: A96563  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
anzen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Rooney, T.; Rowley, D.; Sakano, H.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; PMID:21016719; PMID:11130712  
A;Accession: F95653  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-285 <STO>  
A;Cross-references: GB:A8005173; NID:g10645436; PIDN:AAG21552.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: F9K6.3  
A;Map position: 1  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 47.3%; Score 658.5; DB 2; Length 285;  
Best Local Similarity 50.9%; Pred. No. 8.6e-45;  
Matches 139; Conservative 43; Mismatches 78; Indels 13; Gaps 5;

QY 8 ARRLKGVKALITGGASGIGETTAKLFQHGAKVAIADVDDELGHVSVEAI--GTNST-- 63  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 15 SQRLGKVLTGGATIGSIGSVLRFPKGAQVCIVDQLDDGVBCKSLRGSEKETAF 74  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 64 YTHCDVTNEDGVKNADVNTVSTYGKLDIMFMSNAGISDPNPRIIDNEKADFERVLSNVV 123  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 75 FTGHGVRVEDDISNAVDFAVKNFETDLILNAGLCGAPCPDIRNYSISEFMFTFDVNVK 134  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 124 GVFLCMKHAAVRMIPARSNGIIISTASLGSTWGGSSHAYCGSKHAVLATRNLAIVELGQF 193  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||









C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C/Accession: C70885  
 R/Col: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 399, 537-544, 1998  
 A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
 A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
 A/Reference number: A70500; PMID:98295987; PMID:9634230  
 A/Accession: C70885  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-258 <COL>  
 A/Cross-references: GB:AL008883; GB:AL123456; NID:G3261490; PIDN:CAA15519.1; PID:G261280  
 A/Experimental source: strain H37Rv  
 C/Genetics:  
 A/Gene: RV2857c  
 C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
 F;11-188/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.9%; Score 402.5; DB 2; Length 258;  
 Best Local Similarity 35.8%; Pred. No. 1.5e-24;  
 Matches 91; Conservative 49; Mismatches 105; Indels 9; Gaps 4;

Qy 8 ARLEGGKVALITGGAGIGCTTAKLPSOHGAKVATADVDELGHSHVVEAIGTSNSTVYHC 67  
 Db 5 SQRLAGRVAVITGGSGSIGLAGRRMRAEGATIVGVDDVEAGGADEL---SGLFVPT 61  
 Qy 68 DVTNEDGVKNVNDVNTVSTYKGLDIFMSNAGISDNRPRIIDNEKADFERVLSVNVTVGVL 127  
 Db 62 DVCEDAVGNLPGAAETVGRIDIAFNAGISPPEDNLIENIELAAWRQVDVNLKSVYL 121  
 Qy 128 CMKHAARVMPARSGNIISTASLSSTMGSGSHAYCGSKHVLALTRNLAVELGQFGR 186  
 Db 122 CCRAALRHVMVLAKGSIIVNTAGSVMSATQISYTSKGVILAMRELGVQFQGR 181  
 Qy 187 VNCLSPFGLPTALGKFKGKEEFENVINP-AGNLKGPKEFNVEDVANAALYLASDEAK 245  
 Db 182 VNALCPGPVNTPLQELFARNPERAARMVHVLGRFAEP----DEIAAAVAFILASDDAS 237  
 Qy 246 YVSGHNLFDGGFS 259  
 Db 238 FITASTFLVDGGIS 251

RESULT 15  
 A10406  
 Probable dehydrogenase YPO3351 [imported] - *Yersinia pestis* (strain CO92)  
 C/Species: *Yersinia pestis*  
 C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
 C/Accession: A10406  
 R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
 A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A/Reference number: AB0001; PMID:21470413; PMID:11586360  
 A/Accession: A10406  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-256 <KUR>  
 A/Cross-references: GB:AL590842; PIDN:CAC92581.1; PID:gl15981278; GSPDB:GN00175  
 C/Genetics:  
 A/Gene: YPO3351  
 C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.6%; Score 398; DB 2; Length 256;  
 Best Local Similarity 37.4%; Pred. No. 3.4e-24;  
 Matches 99; Conservative 51; Mismatches 87; Indels 28; Gaps 9;

Qy 5 TAFARLEGKVALITGASGIGETAKLPSOHGAKVATADVDELGHSHVVEAIGTSNSTY 64  
 Db 10 TAFS--LSGKVAITGGATGIGHAELYLAKGARVLMDCADNVA-EIAQLDRDNVAG 66

Qy 65 IHCDVTNEDGVKNVNDVNTVSTYKGLDIFMSNAGIS--DNRPRIIDNEKA---DFERVLS 119  
 Db 67 LHCDVSDSQSVRQVAQAICAFGLDILVNSAGIAALDP-----AEKVREQDWDRITD 119  
 Qy 120 VNVTVGLCMKHAARVMPARSGNIISTASLSSTMGSGSHAYCGSKHVLALTRNLAVE 179  
 Db 120 INLKGVLFCQEVGKHFIQHGKIVNLASQGVVALPNHLAYCASKFGVIGITKVLALE 179  
 Qy 180 LGQFGRVNCLSFGGLPTALGKK-PSGKNEEFENVINPAGNLKGP--KENV-EDVANA 235  
 Db 180 WGPLDIQVNAISTVTVITLALGQKAWSQLAEDM-----KLKIPARRPAYPAEVAAC 230  
 Qy 236 ALYLASDEAKYVSGHNLFDGGFSV 260  
 Db 231 ALFLASDAANMITGENLVIDGGYTI 255

Search completed: October 23, 2003, 12:51:25  
 Job time : 42 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	588.5	42.2	336	1	TS2_MAIZE	P50160 zea mays (m	
2	406	29.1	250	1	LINC_PSEPA	P50197 pseudomonas	
3	396	28.4	255	1	WYFD_BACSU	P39640 bacillus su	
4	381.5	27.4	256	1	Y019_THEMEA	P56318 thermotoga	
5	376	27.0	250	1	LINX_PSEPA	P50198 pseudomonas	
6	366	26.3	260	1	YK02_WYCTU	P10855 mycobacteri	
7	363	26.1	246	1	FABG_THEMEA	Q9x248 thermotoga	
8	357	25.6	248	1	FABG_CHLPM	Q928p2 chlamydia p	
9	346	24.8	251	1	Y325_THEMEA	Q9wyg0 thermotoga	
10	345.5	24.8	261	1	YGCW_ECOLI	P76633 escherichia	
11	343.5	24.7	267	1	LVR_LETAQ	Q91bg2 leifsonia a	
12	341.5	24.5	261	1	DHG_BACSU	P12310 bacillus su	
13	334	24.0	253	1	Y4MP_RHISN	P55575 rhizobium s	
14	332.5	23.9	248	1	FABG_CHLUM	Q9pkf7 chlamydia m	
15	332	23.8	263	1	UCPA_SALTY	P37441 salmonella	
16	329.5	23.7	277	1	LINC_RHOER	Q9ra05 rhodococcus	
17	328.5	23.6	256	1	DHSO_RHOSH	Q59787 rhodobacter	
18	326.5	23.4	247	1	FABG_VIBCH	P38004 chlamydia t	
19	320.5	23.0	244	1	FABG_VIBCH	Q9xgh7 vibrio chol	
20	320.5	23.0	262	1	YBXS_BACSU	P46331 bacillus su	
21	320	23.0	255	1	2BHD_SPREX	P19992 streptomyce	
22	316.5	22.7	244	1	FABG_ECOLI	P25716 escherichia	
23	315.5	22.6	261	1	DHG_EACME	P40288 bacillus me	
24	314.5	22.6	270	1	DHNA_FUAS1	P22441 flavobacter	
25	314.5	22.6	261	1	DHGI_BACME	P39482 bacillus me	
26	313.5	22.5	241	1	FABG_RICRPR	P50941 rickettsia	
27	310	22.3	263	1	UCPA_ECO57	Q8xbj4 escherichia	
28	310	22.3	263	1	UCPA_ECOLI	P37440 escherichia	
29	309.5	22.2	261	1	DHGA_BACME	P10528 bacillus me	
30	308.5	22.1	244	1	FABG_SALTY	O85141 salmonella	
31	308.5	22.1	261	1	DHG2_BACME	P39483 bacillus me	
32	308	22.1	261	1	DHBA_BACSU	P39071 bacillus su	
33	307.5	22.1	244	1	FABG_VIBHA	P55336 vibrio harv	

QY 65 IHCDVTNEDGVKNAVNTYSTY-GKLDIMFSNAGI---SDPNRPRIIDNEKADPERVLSV 120  
 Db 106 VCDVSVEDDVRRAWDALSRGGRLDVTYCNAGVLGRQTAARSILISFDRAEFDRVLRV 165  
 QY 121 NVTGVFLCMKHAARVMIPARSGNIISTASLSTMGSSSHAYCGSKHAYLALTRNLAVEL 180  
 Db 166 NALGAALGKMKHAARAWAPRAGSIVSVASVAALVGLGPHFATSKIAIVGLTAKNAACEL 225  
 QY 181 GQFGIRVNCVLSPPGLPTA-----LGKFKSGIKNEPEFENVI 216  
 Db 226 RAHGVVRVNCVSPRGVATPMLINAWRGHDDATADADRLDLDTVTPSDQVEVKMEVV 285  
 QY 217 NFAGNLKGFNFVEDVANALYLASDEAKYVSGHNLFDIDGFGFVNCNSVI 265  
 Db 286 RGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLI 334

## RESULT 2

LINC\_PSEPA  
 ID LINC\_PSEPA STANDARD; PRT; 250 AA.  
 AC P50197;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)  
 DE (2,5-DIOL dehydrogenase).  
 GN LINC.  
 OS Pseudomonas paucimobilis (Sphingomonas paucimobilis).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
 OC Sphingomonadaceae; Sphingomonas.  
 OX NCBI\_TaxID=13689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UT26;  
 RX MEDLINE=94252977; PubMed=7515041;  
 RA Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;  
 RA "Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol  
 RT dehydrogenase gene involved in the degradation of gamma-  
 RT hexachlorocyclohexane in Pseudomonas paucimobilis";  
 RL J. Bacteriol. 176:3117-3125(1994).  
 CC -1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL  
 CC (2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHO).  
 CC -1- PATHWAY: Gamma-hexachlorocyclohexane degradation; third step.  
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D14595; BAA03444.1; -.  
 CC HSSP: P19992; IHDC.  
 CC InterPro: IPR002198; ADH\_short.  
 CC Pfam: PF00106; adh\_short; 1.  
 CC PRINTS: PR00080; SDRFAMILY.  
 CC PROSITE: PS00061; ADH\_SHORT; 1.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NP\_BIND 9 34 NAD (BY SIMILARITY).  
 FT ACT\_SITE 154 154 BY SIMILARITY.  
 SQ SEQUENCE 250 AA; 25644 MW; PFCICABE47DF789D CRC64;

Query Match 29.1%; Score 406; DB 1; Length 250;  
 Best Local Similarity 37.9%; Pred. No. 3.2e-25;  
 Matches 96; Conservative 42; Mismatches 103; Indels 12; Gaps 6;

QY 11 LEGKVALITGGAGIGETAKLFSQHGAKVATADYQDELGHSHVVEIGTSTNVIHCDVT 70  
 Db 4 LSGKTIIVTGGSGIGRAIVTELLVAGSNVPVADINDENGEAVATSG-GKAAAFRCIDIA 62

QY 71 NEDGVKNVADNTYSTYCKLDIMESNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFLCMK 130  
 Db 63 QEDVKAALVAQTLAAFGGLDGSFNNAAIQAQGLP-LAEVSLERFQSDMDINTVGTFLCMK 121  
 QY 131 HAARWMP-ARSGNIISTASLSTMGSSSHAYCGSKHAYLALTRNLAVELQGFQIRVNC 189  
 Db 122 YQILAMIERGTGKSGIVNTASAGVGVPMHGEVGHAGHAVGLTRVAADYGRGIRNA 181  
 QY 190 LSPFGLPTALGKPKSGIKNE---EEFENVINFAGNLKGFNFVEDVANALYLASDEAKY 246  
 Db 182 LVPQAVTPTMLQR--AMNDNAGLEPYLINSIHPIGRFSEP-----HEQAQAAVWLLSDAASF 235  
 QY 247 VSGHNLFDIDGFGS 259  
 Db 236 VTGSLAADGGFT 248

## RESULT 3

YMPD\_BACSU  
 ID YMPD\_BACSU STANDARD; PRT; 255 AA.  
 AC P39640;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).  
 GN YMPD OR IPA-82D.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=95020537; PubMed=7934828;  
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,  
 RA Hullo M.F., Tonescu M., Lubochinsky B., Marchelino L., Mosser I.,  
 RA Presecan E., Sanson M., Schneider E., Schweizer J., Vertes A.,  
 RA Rapoport G., Danchin A.;  
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97  
 RT kb region from 325 degrees to 333 degrees.";  
 RL Mol. Microbiol. 10:371-384(1993).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kuznetsov F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codari J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.B., Errington J., Fabis C., Fekari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallgren N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G., Guisepi G.,  
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Medina N., Mellado R.P., Mizuno M., Masuda S., Mael C., Medigue C.,  
 RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Noback M.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solido B.,  
 RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosauchi M., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambit R., Wedler E., Wedler H., Weitzenecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus

```
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
DR EMBL; X73124; CAAS1638.1; -.
DR EMBL; Z99123; CAB15799.1; -.
DR PIR; S39737; S39737.
DR HSSP; P50162; IAE1.
DR Subtilist; BG10628; ywFd.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BF88C9B CRC64;

Query Match 28.4%; Score 396; DB 1; Length 255;
Best Local Similarity 36.6%; Pred. No. 2e-24; Indels 16; Gaps 4;
Matches 94; Conservative 48; Mismatches 99;

Qy 11 LEGKVALITGASGIGETTAKLFSQHGAKVAIADVQDELGHVSVEAIGTSTNVIHCDVT 70
Db 5 LTDKTVLITGASGIGYAAVQAFLLQQAQVAVVADIDEAQGEAMVYKKNDRHLHFQTDIT 64

Qy 71 NEDGVKNADVNTVSTYKGLDIFMSNAGIS--DPRNPRIIDNEKADFERVLVSVNVTGVFLC 128
Db 65 DEAAACQHAVESAVHTFGGLDVLINNAGIEIVAP----IHEMELSDWNKVLQVNLTMFLM 120

Qy 129 MKHARVMIIPARSGNIISTASLSTMTGGSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 121 SKHALKHLAKGNIINTCSVGLVAVPDPAPNASKGVLQUTKSNVAVDIKQHQIRVN 180

Qy 189 CLSPFGLPTALGKFKSGIKNEEFENV-----INFAGNLKPKFNVEDVANAALYLASD 242
Db 181 CVCFGIIDTPLNEKSFLENNEGTLEEIKKAKVNPILLRCKP----EEIANVMLFLASD 236

Qy 243 EAKVSGHNLFDIDGFS 259
Db 237 LSSYMTGSAITADGGYT 253

RESULT 4
Y019_THEME
ID Y019_THEME STANDARD; PRT; 256 AA.
AC Q56318;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase TM0019 (EC 1.-.-.-).
GN TM0019.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
[1]

SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE=96125254; PubMed=8550425;
Kletzin A., Adams M.;
"Metabolic and phylogenetic characterization of pyruvate and 2-
ketoglutarate ferredoxin oxidoreductases from Pyrococcus furiosus
and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
J. Bacteriol. 178:248-257(1996).
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RN SEQUENCE FROM N.A.
RP STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
DR EMBL; X85171; CAAS9459.1; -.
DR EMBL; AE001690; AAD35113.1; -.
DR PIR; E72427; E72427.
DR HSSP; O70351; 156W.
DR TIGR; TM0019; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT CONFLICT 130 136 RGGGVII -> TRWRSDH (IN REF. 1).
SQ SEQUENCE 256 AA; 28078 MW; D68160B1D7980C6B CRC64;

Query Match 27.4%; Score 381.5; DB 1; Length 256;
Best Local Similarity 35.7%; Pred. No. 2.9e-23; Indels 11; Gaps 5;
Matches 91; Conservative 54; Mismatches 99;

Qy 11 LEGKVALITGASGIGETTAKLFSQHGAKVAIADVQDELGHVSVEAIGTS--NSTYIHC 68
Db 2 LEGKVAVVTGGQIGGIAIAQLFAENGKVIKVAIDEAGVEREEMLRERGLDVTFFKTD 61

Qy 69 VTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPRNPRIIDNEKADFERVLVSVNVTGVFLC 128
Db 62 VADENSVMKVRKTVETIYGGVDVLNNAVMSVK--SIFERPLEEWEWIRVNLTPYIC 119

Qy 129 MKHARVMIIPARSGNIISTASLSTMTGGSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 120 SRYCAEEMIKRGGGVVIINIASTRAFSQSEPDTEPYASKSGGLVALTHSLAVSLSYHVRV 179

Qy 189 CLSPFGLPTALGKFKSGIKNEE--EPENVINFGNLKPKFNVEDVANAALYLASD- 245
Db 180 SISFGWETSEWKKSLRKXPDLPIDHEQHPAGRVGNPL----DIAHLCVFLADDEKAG 235

Qy 246 YVSGHNLFDIDGFSV 260
Db 236 FITGTNFIVDGGMTV 250

RESULT 5
LIXX_PSEPA
ID LIXX_PSEPA STANDARD; PRT; 250 AA.
AC PS0198;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
DE (2,5-DDOL dehydrogenase).
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DR EMBL; AE001614; AAD18445.1; -.
DR EMBL; AE002207; AAF38299.1; -.
DR EMBL; AF002546; BAA98506.1; -.
DR PIR; D72096; D72096.
DR PIR; H86527; H86527.
DR HSSP; P19992; IHDC.
DR PHCI-2DPAGE; Q9Z8P2; -.
DR TIGR; CP0462; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; Complete proteome.
FT NP BIND 12 36 NADP (BY SIMILARITY).
FT ACT SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26504 MW; 01A2A758B701577E CRC64;

Query Match 25.6%; Score 357; DB 1; Length 248;
Best Local Similarity 33.6%; Pred. No. 2.4e-21;
Matches 87; Conservative 53; Mismatches 92; Indels 28; Gaps 6;

QY 11 LEKVALITGGASGIGETTAKLFSOHGAKVAIADVDDELGHSHVVEAI-GTSNS-TYIHCD 68
DB 5 LVGKVIIVTGGSRGIGLVKFLFENGADVEIWLNERGGQAVIESITGLGGEVSPARVD 64
QY 69 VTHEDGVKNAVDTVSTYKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGLFC 128
DB 65 VSHNGGVKVCQKFLKHKKIDILVNNAGITRDN--LLMRSEDDQSVISTNLSITYT 122
QY 129 MKHAARVMPARGNIIISTASLSSTMGSSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
DB 123 CSSVIRHMKARGSGIINVASIVAKIGSAGQNTYAAAKAGIAITKSLAKEVAARNIRVN 182
QY 189 CLSPFGIPLTALGKFKSGIKNEEFEFNVINFAGNLK-----GPKFNVEDVANAALYL 239
DB 183 CLAPGFT-----ETDMSVLN--DNLKAELWLSIPLGRAGTPEDVARVALFL 227
QY 240 ASDEAKYVSGHNLFDIGGFS 259
DB 228 ASQLSSYMTAQTLLVVDGLT 247

RESULT 9
Y325 THEME STANDARD; PRT; 251 AA.
AC Q9WYGO;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase TM0325 (EC 1.-.-.-).
GN Thermotoga maritima.
OS Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OC NCBI_TaxID=2336;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329 (1999)
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001714; AAD35412.1; -.
DR PIR; G72389; G72389.
DR HSSP; P50162; LAE1.
DR TIGR; TM0325; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP BIND 10 34 NADP (BY SIMILARITY).
FT ACT SITE 152 152 BY SIMILARITY.
SQ SEQUENCE 251 AA; 26635 MW; 61C736A0F13564A5 CRC64;

Query Match 24.8%; Score 346; DB 1; Length 251;
Best Local Similarity 36.9%; Pred. No. 1.8e-20;
Matches 93; Conservative 45; Mismatches 100; Indels 14; Gaps 7;

QY 12 EGKVALITGGASGIGETTAKLFSOHGAKVAIADVDDELGHSHVVEAIGT--SNSTVHCVD 69
DB 4 QGKVLITGASGIGLKAAVWFAERGAIVNDISEKGETVELIKSMGGEAATFGDV 63
QY 70 TNEGCVKNAVDTVSTYKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGLFCM 129
DB 64 AKD--AQIVKVTVEFGRDLILVNNAGIVPYG--NIETSEDFDKTAVNVKGFLLS 119
QY 130 KHAARVMPARGNIIISTASLSSTMGSSSHAYCGSKHVALTRNLAVELGQFGIRVNC 189
DB 130 KYAVEQMKKGGGVNVNVSSEAGLIGIPRCVYSVSKAALLGLTRSLAVDYVDYGIKRNA 179
QY 190 LSPFGLPTALG--KKFSGIKNEEFNFNFAGNLK--GPKFNVEDVANAALYLASDEAK 245
DB 180 VCP--GTTQSEGLMARVKASPNPELLKMTSRIPMKRLGKE---EBIAFAILFAACDEAG 235
QY 246 YVSGHNLFDIGG 257
DB 236 FMTGSIINIDGG 247

RESULT 10
YGCW ECOLI STANDARD; PRT; 261 AA.
AC P76633; P78216; Q46913.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase ygcW (EC 1.-.-.-).
GN YGCW OR B2774.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
CC [2]
CC SEQUENCE OF 1-117 FROM N.A.
CC STRAIN=K12.
CC MEDLINE=97149980; PubMed=9205837;
CC Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
CC Itoh T., Kimura S., Kikagawa M., Makino K., Miki T., Mitsuhashi N.,
CC Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

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RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U29579; AAA69285.1; ALT INIT.
CC EMBL; AE000361; AAC75816.1; ALT INIT.
CC EMBL; D90893; BAA16569.1; ALT_INIT.
CC HSSP; P25529; 1AHH.
CC EcoGene; EG13130; YGCM.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP_BIND 22 46 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 166 166 BY SIMILARITY.
SQ SEQUENCE 261 AA; 28042 MW; 2D6B2382768A4F7E CRC64;

Query Match 24.8%; Score 345.5; DB 1; Length 261;
Best Local Similarity 32.3%; Pred. No. 2.1e-20;
Matches 82; Conservative 58; Mismatches 101; Indels 13; Gaps 6;

Qy 11 LEGKVALITGGASGIGETTAKLFQHGAKVAIADVQDELGHS--VVEAIGTSNSTYIHCD 68
Db LKGTATVTTGNSGLGQAFAMALAKAGANIFIPFVKDNGETKEMIEKQGV-EVDFMQVG 74
Qy 69 VTNEEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNTGVFLC 128
Db ITAEGAPQKIITAACCCERFGTVDIIVNNAGICKLN--KVLDFGRADWPMIDVNLTAAPFL 132
Qy 129 MKHAARVMI PARSGNITSTASLSMTGGSGSHAYCGSKHAVLALTRNLAVELGQFGRVN 188
Db SYBAKIMIPQSKKINICSLFSLYLGQWGPAYSKATHALAGFTKAYCDLGGYNIQVN 192
Qy 189 CLSP--FGLPTALGKFKFSGIRKNEBEFENVINFAGNLKGPKFNVEDVANAALYLASDEAKY 246
Db GIAGFYATDITLATRSNPETNQVRLOHI---PANRWG---DTQDLMAAVFLASPASNY 246
Qy 247 VSGHNLFFIDGFSV 260
Db VNGHLLVVDGGYLV 260

RESULT 11
LVR_LEIAQ
ID -LVR LEIAQ STANDARD; PRT; 267 AA.
AC Q9LBBG2;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Levodione reductase (EC 1.1.1.-) ((6R)-2,2,6-trimethyl-1,4-
DE cyclohexanediol reductase).
GN LVR.
OS Leifsonia aquatica (Corynebacterium aquaticum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=144185;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=M-13;
RX MEDLINE=21281640; PubMed=11388460;
RA Yoshigami A., Wada M., Takagi H., Shimizu S., Nakamori S.;
RT "Cloning, sequence analysis, and expression in Escherichia coli of the
RT gene encoding monovalent cation-activated levodione reductase from
RT Corynebacterium aquaticum M-13.";
RL Biosci. Biotechnol. Biochem. 65:830-836(2001).
RN [2]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=M-13;
RX MEDLINE=99437825; PubMed=10508066;
RA Wada M., Yoshizumi A., Nakamori S., Shimizu S.;
RT "Purification and characterization of monovalent cation-activated
RT levodione reductase from Corynebacterium aquaticum M-13.";
RL Appl. Environ. Microbiol. 65:4399-4403(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND MUTAGENESIS OF GLU-103.
RC STRAIN=M-13;
RX MEDLINE=22638325; PubMed=12621044;
RA Sogabe S., Yoshizumi A., Fukami T.A., Shiratori Y., Shimizu S.,
RA Takagi H., Nakamori S., Wada M.;
RT "The crystal structure and stereospecificity of levodione reductase
RT from Corynebacterium aquaticum M-13.";
RL J. Biol. Chem. 278:19387-19395(2003).
CC -!- FUNCTION: Catalyzes the regio- and stereoselective reversible NAD-
CC dependent reduction of (6R)-2,2,6-trimethyl-1,4-cyclohexanediol
CC (levodione) to (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone
CC (actinol).
CC -!- CATALYTIC ACTIVITY: (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone
CC + NAD(+) = (6R)-2,2,6-trimethyl-1,4-cyclohexanediol + NADH.
CC -!- ENZYME REGULATION: Strongly activated by monovalent cations, such
CC as K(+), Na(+), and NH4(+).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB042262; BAA95121.1; --
CC HSSP; P19992; LHDC
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC Oxidoreductase; NAD.
FT NP_BIND 17 42 NAD (BY SIMILARITY).
FT ACT_SITE 165 165 Role in the determination of
FT ACT_SITE 103 103 stereospecificity.
FT MUTAGEN E->A,D,N,Q: 26-fold increase in Km and a
FT much lower enantiomeric excess of the
FT reaction products.
SQ SEQUENCE 267 AA; 27920 MW; 6F05C89383500304 CRC64;

Query Match 24.7%; Score 343.5; DB 1; Length 267;
Best Local Similarity 33.3%; Pred. No. 3.1e-20;
Matches 88; Conservative 48; Mismatches 105; Indels 23; Gaps 5;

Qy 10 RLEGKVALITGGASGIGETTAKLFQHGAKVAIADVQDE----LGHSVVEAIGTSNSTYI 65
Db 10 RFTDRVVLITGGSGLGRAVLAELAAGAKSLVDVSSEGLEASKAAVLETPDAEVLTT 69
Qy 66 HCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEK---ADFERVLSVW 122
Db 70 VADVDEAQVEAVYVATTFERFRIDGFFNAGLEGKQNP----TESTAAEFQKVSINL 125
Qy 123 TGVFLCMKHAARVMI PARSGNITSTASLSMTGGSGSHAYCGSKHAVLALTRNLAVELGQ 182
Db 126 RGVFLGLEKVLKIMREGSGMVMVTASVGGIRGIGNQSGYAAAKHGVVGLTRNSAVEYGR 185

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CC 183 FGIRVNCLSPFGLPTALGKKF-----SGIKNEEFENVINFAGNLKGPKNVEDVANA 235
CC 186 YGRINAIAPGAIWTPWNSWKQDPNPKAMEEFIOV-----NPSKYGEAPEINAV 240
CC 236 ALYLASDEAKYVSGHNLFDIGGFS 259
CC 241 VAFLLSDASYVNTATVVPIDGGQS 264

RESULT 12
DHG_BACSU STANDARD; PRT; 261 AA.
ID DHG_BACSU
AC P12310; P94430;
DT 01-OCT-1989 (Rel. 12, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucose 1-dehydrogenase (EC 1.1.1.47).
GN GDH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168021; PubMed=3082854;
RA Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.;
RT "Characterization of the developmentally regulated Bacillus subtilis
RL glucose dehydrogenase gene.";
RN J. Bacteriol. 166:238-243 (1986).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=971124189; PubMed=8969502;
RA Yamane K., Kumano M., Kurita K.;
RT "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome:
RL determination of the sequence of a 146 kb segment and identification
RL of 113 genes.";
RN Microbiology 142:3047-3056 (1996).
RP [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Noszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boutsier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Enrich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Seiguchi J., Sekowska A., Serrero S.J., Serrero P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Sorokin A., Tacconi E., Tanaka T., Terstra P., Tognoni A.,
RA Tobato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
RA Viari A., Wambut R., Wedler E., Wedler K., Yasunaga K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunaga K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RN Nature 390:249-256 (1997).

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CC 183 FGIRVNCLSPFGLPTALGKKF-----SGIKNEEFENVINFAGNLKGPKNVEDVANA 235
CC 186 YGRINAIAPGAIWTPWNSWKQDPNPKAMEEFIOV-----NPSKYGEAPEINAV 240
CC 236 ALYLASDEAKYVSGHNLFDIGGFS 259
CC 241 VAFLLSDASYVNTATVVPIDGGQS 264

RESULT 13
Y4MP_RHISN STANDARD; PRT; 253 AA.
ID Y4MP_RHISN
AC P55575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative short-chain type dehydrogenase/reductase Y4MP (EC 1.1.1.47).
GN Y4MP.
OS Rhizobium sp. (strain NGR234).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;

Query Match 24.5%; Score 341.5; DB 1; Length 261;
Best Local Similarity 34.4%; Pred. No. 4.4e-20;
Matches 93; Conservative 50; Mismatches 98; Indels 29; Gaps 10;

QY 11 LEGKVALITGASGIGETTAKLFSQHGAKVAI---ADVQD--ELGHSVVEAIGTNSVTI 65
DB 5 LKGKVAITGAASGLGKAMAREFCKEQAKVINYKQDPNEVKEVIAKGG--EAVV 62
QY 66 HCDVTNEDGVKNAVNTVSTYKLDIMFNSNAGISDENRRIIDNEK--ADFERVLSVNT 123
DB 63 QGDVTKBEDVKNIQVQTAIKFEGTLDIMINNALENP---VPSHEMPLKDWKVTGNT 118
QY 124 GVFLCMKHARVMIPAR-SGNIITSTASLSTMGSGSHAYCGSKHVALALTRNLAVELQ 182
DB 119 GAFLGSREAIKYFVENDIKGNVINMSSVHEVIPWPLFVHYAASKGIGIKLMTTLEAYP 178
QY 193 FGIRVNCLSPFGLPTAL-GKKGSGIKNEEFENVINFAGNLKGPKNVEDVANAALYLAS 241
DB 179 KGIRVNNIGPGAINTPINAEKPADPKQKADVESNIPM-GYIGEP----BEIAVAWLAS 233
QY 242 DEAKYVSGHNLFDIGGFSVCSNVKVPQYP 271
DB 234 KEASVYTGITLFDGGMT-----QYP 254

RESULT 13
Y4MP_RHISN STANDARD; PRT; 253 AA.
ID Y4MP_RHISN
AC P55575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative short-chain type dehydrogenase/reductase Y4MP (EC 1.1.1.47).
GN Y4MP.
OS Rhizobium sp. (strain NGR234).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;

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RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
 RA Perret X.;  
 RA "Molecular basis of symbiosis between Rhizobium and Legumes.";  
 RL Nature 387:394-401(1997).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY. HIGH, TO BACTERIAL FABG.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; AE000085; AAB91779.1; -;  
 DR HSPF; P29132; 1DPI.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Hypothetical protein; Oxidoreductase; Plasmid.  
 FT NP\_BIND 10 35 NAD OR NADP (BY SIMILARITY).  
 FT ACT\_SITE 159 159 BY SIMILARITY.  
 SQ SEQUENCE 253 AA; 25994 MW; B8208A0B0F5P542F CRC64;  
 Query Match 24.0%; Score 334; DB 1; Length 253;  
 Best Local Similarity 34.2%; Pred. No. 1.7e-19;  
 Matches 90; Conservative 55; Mismatches 92; Indels 26; Gaps 10;  
 QY 11 LEGKVALITGAS--GIGETTAKLPSHQKAKVAIADVQ--DELGHSVVEAIGTSNITYI-- 65  
 DB 3 LKGTAVTSGAASXRGIGRATAELFASHGARVAILDINADEAKAAGDLPVHGAIHGL 62  
 QY 66 HCDVTNEDGVKNVADNTVSTYCKLIDMFSNAGISDPNRPRIIDNEKADFERVLSVNTGV 125  
 DB 63 RCDVADRASCTSSASDEVLSAFGVANILINNAQTQP--VKTLDTSDDAQWRIVAVNMTGV 120  
 QY 126 FLCMKHAARVMIPAR---SQNIISTASLSSTMGGG--SSHAYCGSKHAVIALTRNLAVE 179  
 DB 121 L-----NLSQVFIPNWRONGGSIACMSVSQRGGGIFGGPHYSAAKAGVLGLAKAWARE 176  
 QY 180 LGQFGIRVNCUSPFLPTAL--GKFGSGIKNEEFENV--INFAGNLKGFKNFVEDVANAAL 237  
 DB 177 FGPDRIWNCVTPGLQTDITGDKLSAEMRADIVKGIPLSLRGDAR-----DVANIYL 229  
 QY 238 YLASDEAKYVSGHNLFDIDGGFSV 260  
 DB 230 FLASDL SAYVTGAVIDVNGGMLI 252  
 RESULT 14  
 FABG\_CHLMU STANDARD; PRT; 248 AA.  
 AC Q9PKF7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-  
 DE acyl carrier protein reductase).  
 GN FABG OR TC0508.  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MoPn / Nigg; PubMed=10684935;  
 RC MEDLINE=20150255;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RL Pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.  
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.  
 CC -----  
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 CC -----  
 DR EMBL; AE002319; AAF39350.1; -;  
 DR PIR; E81695; E81695.  
 DR HSPF; P50163; 2AE1.  
 DR TIGR; TC0508; -;  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
 FT NP\_BIND 12 36 NADP (BY SIMILARITY).  
 FT ACT\_SITE 157 157 BY SIMILARITY.  
 SQ SEQUENCE 248 AA; 25977 MW; 1F5C8968CB05FF58 CRC64;  
 Query Match 23.9%; Score 332.5; DB 1; Length 248;  
 Best Local Similarity 32.9%; Pred. No. 2.1e-19;  
 Matches 85; Conservative 52; Mismatches 98; Indels 23; Gaps 7;  
 QY 11 LEGKVALITGASGIGETTAKLPSHQKAKVAIADVQDELGHSVVEAIGT---SNSTYIHC 67  
 DB 5 LVNKAATVTSYCKLIDMFSNAGISDPNRPRIIDNEKADFERVLSVNTGV 64  
 QY 68 DVTNEDGVKNVADNTVSTYCKLIDMFSNAGIS--DPNRPRIIDNEKADFERVLSVNTGV 126  
 DB 65 DVSKNDVSAQVKFAEYGTIDVVNNAGITDLSLMRSEEE---WSSVIDTNLSIY 121  
 QY 127 LCMKHAARVMIPARSGNIISTASLSSTMGGSSHAYCGSKHAVIALTRNLAVELQPGFIR 186  
 DB 122 NVCSAVIRPMIKARSGAIVNMISSIVLGRSGPGQNTYAAKAGIIGFSKALSKEVGSKNIR 181  
 QY 187 VNCUSPFLPTALGKFS--GIKNEEFENVINPAGNLKGFKNV---EDVANAALYLAS 241  
 DB 182 VNCIAPGFIDTDMTCKGLSDNLKNEW-----LKGVPGLGRVGTPEEIAAALFLAS 230  
 QY 242 DEAKYVSGHNLFDIDGGFS 259  
 DB 231 NQSSYITGQVLSVDGWA 248  
 RESULT 15  
 UCPA\_SALTY STANDARD; PRT; 263 AA.  
 ID UCPA\_SALTY  
 AC P37441;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Oxidoreductase ucpa (EC 1.-.-).  
 GN UCPA OR STM2445 OR STY2682 OR T0413.  
 OS Salmonella typhimurium, and  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602, 601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium; STRAIN=L22 / SGSC1412 / ATCC 700720;  
 RC MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RA "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
RT L72.";  
RL Nature 413:852-856 (2001).  
RN [2]  
RP SEQUENCE OF 204-263 FROM N.A.  
RC SPECIES=S.typhi; STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RY Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrett B.G.;  
RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
RT enterica serovar Typhi CT18.";  
RL Nature 413:848-852 (2001).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12544504;  
RY Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2  
RT and CT18.";  
RL J. Bacteriol. 185:2330-2337 (2003).  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.  
CC -----  
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CC -----  
CC DR EMBL; AE008910; AL21339.1; -;  
CC DR EMBL; AL627274; CAD07676.1; -;  
CC DR EMBL; AE016835; AO68131.1; -;  
CC DR F01; A38121; A38121.  
CC DR StyGene; SG10424; ucPa.  
CC DR InterPro; IPR002198; ADH\_short.  
CC DR Pfam; PF00106; adh\_short; 1.  
CC DR PRINTS; PR00080; SDRFAMILY.  
CC DR PROSITE; PS00061; ADH\_SHORT; FALSE\_NEG.  
CC KW Oxidoreductase; Complete proteome.  
CC NP BIND 10 32 NAD OR NADP (BY SIMILARITY).  
CC FT ACT SITE 155 155 BY SIMILARITY.  
CC FT CONFLICT 218 218 L -> M (IN REF. 2).  
CC FT CONFLICT 258 258 S -> T (IN REF. 2).  
CC FT CONFLICT 263 263 V -> I (IN REF. 2).  
CC SQ SEQUENCE 263 AA; 27870 MW; 81B26CAD9B4D534E CRC64;

Query Match 23.8%; Score 332; DB 1; Length 263;  
Best Local Similarity 33.1%; Pred. No. 2.5e-19;  
Matches 87; Conservative 49; Mismatches 113; Indels 14; Gaps 5;

QY 10 RLEKGVALTGASGIGETTAKFLSQHAKVADVDQDELGHSHVVEAIGTSN-STYIHC 68  
Db 3 KLTKTALITCASOGIGEGIARVFARHGANLILDIISDEIKLDELGGRGHRCCTAVKAD 62  
QY 69 VTNEDGVKNVADNTVSTYKLDIMFSNAGISDPNRPRIIDNEKADPFERVLNVVTGVFLC 128  
Db 63 VRDFASVQAAVARAKETEGRIDILVNNAGVCRNLGNFLDMSEEDRDPH--IDINIKGVNV 120  
QY 129 MKHAARVMIPARSGNIISTASLSSTW-GGSSSHAYGSKHVLATRLNLADELGGGGRV 187  
Db 121 TKAVLPWKIKKQGRIVMSSVTGDMVADPGETAYALSAAIVGLTKSLAVEYAGSGIRV 180  
QY 188 NCLSPFGLPTALGKKKSGIKNEEFENVNFAG-----NLKGPKNVEDVANAALYLAS 241  
Db 181 NAICPGVIRTPMAESTARQNPDPPESVITEMAKAIPRLRLADPL-----EVELAAFLAS 236  
QY 242 DEAKYVSGHNLFDIDGFGFSCNSV 264  
Db 237 DESSYLTGTQNVIDGGSTLPESV 259

Search completed: October 23, 2003, 12:48:56  
Job time : 26 secs

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1364	97.9	277	10	Q94KL7		Q94KL7 forsythia i
2	734	52.7	267	10	P93697		P93697 vigna ungu
3	700.5	50.3	271	10	Q94G09		Q94G09 cucumis sat
4	695	49.9	274	10	Q8HD09		Q8HD09 phaseolus l
5	693.5	49.8	271	10	Q94G10		Q94G10 cucumis sat
6	685	49.2	284	10	Q50038		Q50038 nicotiana t
7	677	48.6	284	10	Q82465		Q82465 ipomoea tri
8	673	48.3	277	10	Q9SBD8		Q9SBD8 ipomoea tri
9	670	48.1	284	10	Q9SBD6		Q9SBD6 ipomoea tri
10	668	48.0	277	10	Q9SBD7		Q9SBD7 ipomoea tri
11	665.5	47.8	273	10	Q9SBN0		Q9SBN0 citrullus l
12	658.5	47.3	285	10	Q9C826		Q9C826 arabidopsis
13	652.5	46.8	278	10	Q94KL8		Q94KL8 podophyllum
14	625.5	44.9	303	10	Q9SCU0		Q9SCU0 arabidopsis
15	597.5	42.9	283	10	Q9ZR17		Q9ZR17 arabidopsis
16	593.5	42.6	259	10	Q93Y47		Q93Y47 digitalis l

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QY 62 STYIHCDVTNEDGVKNAVDNTYSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVN 121
DB 66 STYIHCDVTNEDGVKNAVDNTYSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVN 125
QY 122 VTGVFLCMKHAARVMIIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLAVELG 181
DB 126 VTGVFLCMKHAARVMIIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLAVELG 185
QY 182 QFGRVNCISPFGLPTALGKKGSGIKNEEFENVINFAGNLKGPKNFVEDVANAALYAS 241
DB 186 QFGRVNCISPFGLPTALGKKGSGIKNEEFENVINFAGNLKGPKNFVEDVANAALYAS 245
QY 242 DEAKYVSGHNLFTDGGFSVCNSVIKVFQYDPS 273
DB 246 DEAKYVSGHNLFTDGGFSVCNSVIKVFQYDPS 277

RESULT 2
P93697 PRELIMINARY; PRT; 267 AA.
AC P93697;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE CPRD12 protein.
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3917;
RN [1]
RP SEQUENCE FROM N.A.
RA Iuchi S., Yamaguchi-Shinozaki K., Urao T., Shinozaki K.;
RT "Characterization of two cDNAs for novel drought-inducible genes in
RT the highly drought-tolerant cowpea.";
RL J. Plant Res. 109:415-424(1996).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; D88121; BAAL3541.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 267 AA; 28484 MW; 8C4A4A2E9F41B64 CRC64;

Query Match 52.7%; Score 734; DB 10; Length 267;
Best Local Similarity 56.3%; Pred. No. 1,1e-47;
Matches 147; Conservative 41; Mismatches 67; Indels 6; Gaps 2;

QY 9 RLREGKVALITGASGIGETTAKLFSQHCAGKVAIADVODELGHSHVVEAIGTSYIHCD 68
DB 12 KRLEGKVALITGASGIGETTAKLFSQHCAGHVVVADIQDDVGLSLCNEL--KSAIYVHCD 69
QY 69 VTNEDGVKNAVDNTYSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVNVTGVFLC 128
DB 70 VTKEEDIEKCVDTAVSKPKGLDIMPFSNAGTDFPKKSILDNKTSDFERVISVNLVGPFLG 129
QY 129 MKHAARVMIIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
DB 130 TKHAARVMIIPARSGNIISTASVAGCTGGGATHAYTSSKHALVGLTKNTAVELGQFGIRVN 189
QY 189 CLSPFGLPTALGKKGSGIKNEEFENVINFAGNLKGPKNFVEDVANAALYASDEAKYVS 248
DB 190 CVSPFPAITVTPLLNKYFNLEDEGVRKTYMNLKGVPVP---NDVAEALYASDESKFVS 245
QY 249 GHNLFTDGGFSVCNSVIKVFQ 269
DB 246 SHNLVIDGGGLINSVGFPMFE 266

RESULT 3

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Q94G09 PRELIMINARY; PRT; 271 AA.
ID Q94G09;
AC Q94G09;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Sex determination protein.
GN CSG.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RA Sun J.-O., Li Q.-Z., Li X.-G.;
RT "Gene cloning and expression of CSG in cucumber.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF286651; AAK80306.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 271 AA; 28997 MW; 7CD6ED7F52AD6224 CRC64;

Query Match 50.3%; Score 700.5; DB 10; Length 271;
Best Local Similarity 53.7%; Pred. No. 3.7e-45;
Matches 146; Conservative 44; Mismatches 75; Indels 7; Gaps 4;

QY 1 MOLTAFAARLEGKVALITGASGIGETTAKLFSQHCAGKVAIADVODELGHSHVVEAIGTS 60
DB 3 IQLPATAARLEGKVAITGATGIGETAKLFSQHCAGKVAIADVODELGHSHVVEAIGTS 62
QY 61 NSTYIHCDVTNEDGVKNAVDNTYSTYKGLDIMPFSNAGI--SDPNRPRIIDNEKADPERVL 118
DB 63 SSVFVHCDVTKEKDVETAVDTAVSKYKGLDIMPFSNAGI--SDPNRPRIIDNEKADPERVL 121
QY 119 SVNVTGVFLCMKHAARVMIIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNLAV 178
DB 122 NVNLVGAFPLGTPKHAARVMIIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVALTRNA 181
QY 179 ELGQFGIRVNCISPFGLPTALGKKGSGIKNEEFENVINFAGNLKGPKNFVEDVANAAL 237
DB 182 DLGRYGRVNCISVNVVPTTEMGRKLPKVDGGGEP--SFYMSLKNGLDILREEDVGEAVV 238
QY 238 YLASDEAKYVSGHNLFTDGGFSVCNSVIKVFQ 269
DB 239 YLGDESKVCVSGNLIVDGGFTVVNQALCSFR 270

RESULT 4
Q8H0D9 PRELIMINARY; PRT; 274 AA.
ID Q8H0D9;
AC Q8H0D9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alcohol dehydroge.
GN ADH.
OS Phaseolus lunatus (lima bean) (Phaseolus limensis).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3884;
RN [1]
RP SEQUENCE FROM N.A.
RA Horiuchi J., Arimura G., Ozawa R., Muroi A., Takabayashi J.,
RA Nishioka T.;
RT "Phaseolus lunatus.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

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[illegible]





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Query Match      48.1%; Score 670; DB 10; Length 284;
Best Local Similarity 51.7%; Pred. No. 8.1e-43;
Matches 134; Conservative 41; Mismatches 84; Indels 0; Gaps 0;

QY 9 RRLEGGKVALITGGASGIGETTAKLFSQHGAKVAIADVDQDELGHVSVEAIGTSNSTYIHCD 68
Db 12 KRLEGGKVALITGAANGIGATTARLFAQHCKVKIIADDDKNGSLUSVAEEIGPEYALFHCD 71
QY 12 KRLEGGKVALITGAANGIGATTARLFAQHCKVKIIADDDKNGSLUSVAEEIGPEYALFHCD 71
Db 72 VRIESDVQNAVDTTVSRYGKLDIMFNSAGVAGSDTTSILEASPENINLVFETNVFGAFC 131
QY 129 MKHAARVMI PARSGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 132 AKHAARVMI PARKGVSIFSAASEVFGITSDDTYSKCAVVGKSLCVMEMKYGIKAN 191
QY 189 CLSPFGLPTALGKFKSGIKNEEFENVINPAGNLKGPKNVEDVANAALYLASDEAKYVS 248
Db 192 CVSPYVILTKLGMIMPTQDKLAEIIVAEASNFKGTLLTTEDVAAALYLADGSKFVS 251
QY 249 GHNLFDIDGFGSVCNSVIK 267
Db 252 GLNLLIDGGFTTTNTAFQV 270

RESULT 10
Q9SBD7 ID Q9SBD7 PRELIMINARY; PRT; 277 AA.
AC Q9SBD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Short-chain alcohol dehydrogenase (S-locus linked stigma
DE protein).
DE SPP OR SSP10.
GN Ipomoea trifida.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Teuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT "S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=H77-2;
RC Teuchiya T., Suabe K., Wataae T., Kagaya Y., Koyama Y.;
RT "Characterization of promoter region of the SSP gene from Ipomoea
RT trifida regulates stigma-specific expression.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072449; AAC35342.1; -.
DR EMBL; AB070221; BAB86916.1; -.
DR HSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 277 AA; 29257 MW; A0CDB434B31C666D CRC64;

Query Match      48.0%; Score 668; DB 10; Length 277;
Best Local Similarity 51.7%; Pred. No. 1.1e-42;
Matches 134; Conservative 41; Mismatches 84; Indels 0; Gaps 0;

QY 9 RRLEGGKVALITGGASGIGETTAKLFSQHGAKVAIADVDQDELGHVSVEAIGTSNSTYIHCD 68
Db 12 KRLEGGKVALITGAANGIGATTARLFAQHCKVKIIADDDKNGSLUSVAEEIGPEYALFHCD 71
QY 69 VTNEDGVKNAVDTTVSTYKLDIMFNSAGISDPRPRIIDNEKADFERVLSVNVTVGFLC 128
Db 72 VRIESHVQHAVDTVSRYGKLDIMFNSAGVAGSDTTSILEASPENINLVFETNVFGAFC 131
QY 129 MKHAARVMI PARSGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 132 AKHAARVMI PARKGVSIFSAASEVFGITSDDTYSKCAVVGKSLCVMEMKYGIKAN 191
QY 189 CLSPFGLPTALGKFKSGIKNEEFENVINPAGNLKGPKNVEDVANAALYLASDEAKYVS 248
Db 192 CVSPYVILTKLGMIMPTQDKLAEIIVAEASNFKGTLLTTEDVAAALYLADGSKFVS 251
QY 249 GHNLFDIDGFGSVCNSVIK 267
Db 252 GLNLLIDGGFTTTNTAFQV 270

RESULT 11
Q9SBD7 ID Q9SBD7 PRELIMINARY; PRT; 273 AA.
AC Q9SBD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Wt62L.
GN WTS2L.
OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=3654;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J., Kang H., Jun S., Lee J., An G.;
RT "Cloning of three gibberellin-regulated cDNAs from watermelon during
RT early seed development: down-regulated one cDNA and up-regulated two
RT cDNAs.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AB018559; BAA89230.1; -.
DR HSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 273 AA; 28835 MW; 904A835DD52B6E2 CRC64;

Query Match      47.8%; Score 665.5; DB 10; Length 273;
Best Local Similarity 51.1%; Pred. No. 1.7e-42;
Matches 137; Conservative 48; Mismatches 74; Indels 9; Gaps 4;

QY 9 RRLEGGKVALITGGASGIGETTAKLFSQHGAKVAIADVDQDELGHVSVEAIGTSNSTYIHCD 68
Db 11 RRLDGKVALITGGASGIGTSVAVRIFHENGAKVIAIDQDEIGQKIADLG-DDVSYIHCD 69
QY 69 VTNEDGVKNAVDTTVSTYKLDIMFNSAGISDPRPRIIDNEKADFERVLSVNVTVGFLC 128
Db 70 VSKEDDVSNLVDAAVHRHGKLDIMYAGVLDLRSFGILDVTKSLDKVLGVNVMGAFWG 129
QY 129 MKHAARVMI PARSGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 130 AKHAARVMI PEKNGCILFTSSATTNTAGLSSHYPYAAKCAVLGLVRNLAAELGQHGIRVN 189
QY 189 CLSPFGLPTALGKFKSGIKN---EEEFENVINPAGNLKGPKNVEDVANAALYLASDEAK 245
Db 190 CVAPFVVATGI----AGSRDPMQAEALETWTTWNLKGRVLKADDIKAAALYLASDDAN 245
QY 246 YVSGHNLFDIDGFSVCN-SVIKVFQYPD 272
Db 246 YVSGNLVVDGGYVNVNPTMLTKLMD 273

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RESULT 12
Q9C826 PRELIMINARY; PRT; 285 AA.
ID Q9C826;
AC Q9C826;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Short chain alcohol dehydrogenase, putative (Short-chain
DE dehydrogenase/reductase).
GN F19K6_3 OR ABA2 OR ATIG52340.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC Ericaceae II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=5702;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altaki H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gall J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militecher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Unterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana";
RL Nature 408:816-820 (2000).
[2]
RP SEQUENCE FROM N.A.
RA Cheng W.-H., Endo A., Zhou L., Penney J., Chen H.-C., Arroyo A.,
RA Leon P., Nambara E., Asami T., Seo M., Koshiba T., Sheen J.;
RA "A unique short-chain dehydrogenase/reductase in Arabidopsis glucose
RA signaling and abscisic acid biosynthesis and functions.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL; AC037424; AAC51536.1; -
CC EMBL; AY082344; AAL99237.1; -
CC EMBL; AY082345; AAL99238.1; -
CC EMBL; AY095603; AAM20454.1; -
CC HSP; P29132; IDFI
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC Oxidoreductase.
KW NON TER 278
SQ SEQUENCE 285 AA; 30272 MW; 8B555DAED736DF4 CRC64;
Query Match 47.3%; Score 658.5; DB 10; Length 285;
Best Local Similarity 50.9%; Pred. No. 66-42; Mismatches 13; Gaps 5;
Matches 139; Conservative 43; Indels 13;

QY 8 ARLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSHVVEAI--GTSNST-- 63
DB 15 SQRLLGKVALITGGATGIGESIVRLFKHGAKVCIVLQDDDLGGVCKSLRGSKETAF 74
QY 64 YHCDVTNEDGVKNADVNTSTYTKLDMFMSNAGISDPNRPRIIDNEKADFRLVSNVVT 123
DB 75 FHGDVVRVEDDISNADVDFAVKNFGTLDILINNAGLCGAPCPDIRNYSLSSEFMTFDVNVK 134
QY 124 GVFLCMKHAARVMI PARSGNIISTASSTMTGGSSSHAYCGSKHAVLALTRNLAVELGQF 183
DB 135 GAFLSMKHAARVMIPEKKGSIVSLCSVGGVGVGPHSYVSGSKHAVLGLTRSAALGQH 194
QY 184 GIRVNCLSFPGPTALGKKFKSGIKNEEFENVI----NFA----GNLKGPKFNVEDVANAA 236
DB 195 GIRVNCVSPYAVATKLA--LAHLPEERTEDAFVGRFAAANANLKGVELTVDDVANAV 252
QY 237 LYLASDEAKYVSGHNLFIIDGGFCVNSVVKYQF 269
DB 253 LFLASDDSRVYISGDNLMIDGGFTCTNHSFKVFR 285

RESULT 13
Q94KL8 PRELIMINARY; PRT; 278 AA.
ID Q94KL8;
AC Q94KL8;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Rhizome secoisolariciresinol dehydrogenase (Fragment).
DE Podophyllum peltatum (Mayapple).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Berberidaceae; Podophyllum.
OX NCBI_TaxID=35933;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21201084; PubMed=11278426;
RA Xia Z.Q., Costa M.A., Pelissier H.C., Davin L.B., Lewis N.G.;
RA "Secoisolariciresinol Dehydrogenase Purification, Cloning, and
RA Functional Expression. IMPLICATIONS FOR HUMAN HEALTH PROTECTION.";
RL J. Biol. Chem. 276:12614-12623 (2001).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL; AF352734; AAK38664.1; -
CC InterPro; IPR002198; ADH_short.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC Oxidoreductase.
KW NON TER 278
SQ SEQUENCE 278 AA; 29253 MW; DB735A376E112375 CRC64;
Query Match 46.8%; Score 652.5; DB 10; Length 278;
Best Local Similarity 52.2%; Pred. No. 1.7e-41;
Matches 133; Conservative 43; Mismatches 76; Indels 3; Gaps 3;

QY 10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSHVVEAIGTSN-STYIHD 68
DB 13 RLQDKVAIITGGAGGIGETTAKLFSYRGAKVIAADHGGKVCNNIGSPDIVSFVHCD 72
QY 69 VTNEDGVKNADVNTSTYTKLDMFMSNAGISDPNRPRIIDNEKADFRLVSNVTVGFLC 128
DB 73 VTNEDVRNLVDTTIAKHGKLDIMEGNVGLSTTTPSYILEAGNEDFKRVMIDINVYGAFLV 132
QY 129 MKHAARVMI PARSGNIISTASLS--TMGGGSHAYCGSKHAVLALTRNLAVELGQFGRV 187
DB 133 AKHAARVMI PAKGSI VFTASISSSTAGEGSHVYATKHAVLGLTSLCTELGEYGRV 192
QY 188 NCLSPGLPTALCKKPSGIGTNEEFENVI--NFA----GNLKGPKFNVEDVANAAVLASDEAKYV 247
DB 193 NCVSPYIVASPLTDFGVG--DSRVEELAHQAANLKLRAEDVADAVAYLAGDESKYV 251

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Qy 248 SGHNLFDGGSVCN 262
Db 252 SGLNLVDGGVTRTN 266

RESULT 14
Q9SCU0 PRELIMINARY; PRT; 303 AA.
AC Q9SCU0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Short-chain alcohol dehydrogenase-like protein.
GN T18N14.60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K.,
RA Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,
RA McCombie W.R.;
RT "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cM.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AC005275; AAD14442.1; -.
DR EMBL; AL161496; CAB77799.1; -.
DR HSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 283 AA; 29994 MW; 93B0A97CECC859BC CRC64;

Query Match 42.9%; Score 597.5; DB 10; Length 283;
Best Local Similarity 47.0%; Pred. No. 2.4e-37;
Matches 126; Conservative 45; Mismatches 86; Indels 11; Gaps 4;

Qy 9 RRLGKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHSHVVEAIGTSYIHCD 68
Db 16 RKEGKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHSHVVEAIGTSYIHCD 74
Qy 69 VTNEDGKNAVDNTVSTYGLDIFMSNAGISDPNRPRIIDNEKADPERVLSVNVGVFLC 128
Db 75 VTKESDIANAVDFAVSLHTKLDIMYNNAGIPCKTPPSIVDLNVPDKVINTNVRGVMA 134
Qy 129 MKHAARVMIIPARSGNTIISTASLSSTMGSGSHAYCGSKHAVLALTRNLAVELGQFIRVN 188
Db 135 IKHAARVMIIPRNSGSIICAGSVTGMGLAQHTYSVSKSAVIGIVRSTASELCKHRIRVN 194
Qy 189 CLSPPLGPTA-----LGKPSGINKBEEFENVINFAGNLKGPKFNVEDVANAALYLASDE 243
Db 195 CISPPFAITTSFVMDENRQIYPGV-DBSRLTIQIVQSTGVLNGVECEPTDVANAAYLASDD 253
Qy 244 AKYVSGHNLFDGGSVCNVIKVFQYP 271
Db 254 SKYVNGHNLVVDGGF-----TTVKTLDPP 277

Search completed: October 23, 2003, 12:50:40
Job time : 101 secs

Qy 5 TAFARLEGKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHSHVVEAIGTSYST- 63
Db 26 TLYPRLEGKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHSHVVEAIGTSYST 85
Qy 64 ---YHCDVTNEDGKNAVDNTVSTYGLDIFMSNAGISDPNRPRIIDNEKADPERV 118
Db 86 MVAFISCDVSEADENLVNVTARYGRDLILFNAGVLDGDKKHSILDFDADEFDHYM 145
Qy 119 SVNVTGFLCKHARVMIIP-ARSGNIISTASLSSTMGSGSHAYCGSKHAVLALTRNLA 177
Db 146 RVNRYGVGLGKMGHARMIKRGFKGCIISTASVAGVGMGMGPHTAYTASKEAIVGLTKNA 205
Qy 178 VELGQFGRVNCISLPGFLPTAL----GKKPSG--LKNE--EEFENVINFAGNLKGPKFNV 229
Db 206 CELGKGRVNCISLPGFVATSMVNWARKTSGGVDDEDDVEEEMEEFVRSANLKGKTLRA 265
Qy 230 EDVANAALYLASDEAKTVSGHNLFDGGSVCNVI 265
Db 266 NDIAEAALYLASDESKYVNGHNLVVDGGVITARNCV 301

RESULT 15
Q9ZR17 PRELIMINARY; PRT; 283 AA.
AC Q9ZR17;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative alcohol dehydrogenase.

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